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## (57) Abstract

A method of modulating the ripening and/or senescence characteristics in plants of the genus *Musa* comprises transforming plants with one or more sequences obtainable from the deposited cDNA library having the accession number 40184, regenerating said plants and selecting from the population of transformants those plants having modulated and/or tissue senescence characteristics.

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### GENETIC CONTROL OF FRUIT RIPENING

This invention relates generally to the modification of a plant phenotype by the regulation of plant gene expression. More specifically it relates to the modulation of the ripening and/or tissue senescence characteristics and plants derived therefrom. One suitable application of the present invention is the modulation of ripening and/or senescence processes in plants of the genus *Musa* (referred to herein as banana).

Two principal methods for the control of expression are known, viz.: overexpression and underexpression. Overexpression may be achieved by insertion of one or more than one extra copies of the selected gene. It is, however, not unknown for plants or their progeny, originally transformed with one or more than one extra copy of a nucleotide sequence, to exhibit the effects of underexpression as well as overexpression.

For underexpression, often referred to as "gene silencing", there are two principle methods which are commonly referred to in the art as "antisense downregulation" and "sense downregulation (also referred to as "cosuppression"). Both of these methods lead to an inhibition of expression of the target gene. Other lesser used methods involve modification of the genetic control elements, the promoter and control sequences, to achieve greater or lesser expression of an inserted gene.

There is no reason to doubt the operability of these methods: they are well-established, used routinely in laboratories around the world and products in which they have been used are on the market.

Gene control by any of these methods requires the insertion of a selected gene or genes into plant material which can be regenerated into plants. This transformation process can be performed via a number of methods, for example: the *Agrobacterium*-mediated transformation method.

In the microparticle bombardment method, microparticles of dense material, usually gold or tungsten, are fired at high velocity at the target cells where they penetrate the cells, opening an aperture in the cell wall through which DNA may enter. The DNA may be coated on to the microparticles or may be added to the culture medium.

In microinjection, the DNA is inserted by injection into individual cells via an ultrafine hollow needle.

Another method, viz. fibre-mediated transformation, applicable to both monocots and dicots, involves creating a suspension of the target cells in a liquid, adding microscopic needle-like material, such as silicon carbide or silicon nitride "whiskers", and agitating so that the cells and whiskers collide and DNA present in the liquid enters the cell.

5 In summary, then, the requirements for both sense and antisense technology are known and the methods by which the required sequences may be introduced are known. What remains, then is to identify genes whose regulation will be expected to have a desired effect, isolate them or isolate a fragment of sufficiently effective length, construct a chimeric gene in which the effective fragment is inserted between promoter and termination signals, and insert the  
10 construct into cells of the target plant species by transformation. Whole plants may then be regenerated from the transformed cells.

Bananas are a globally important fruit crop. They are not only a popular dessert fruit, but represent a vital carbohydrate staple in the tropics with as many as 100 million people  
15 subsisting on bananas and plantains as their main energy source. The cultivated dessert banana is commonly triploid, parthenocarpic and belongs to the *Musa* AAA genome group, eg. Cavendish subtypes. Bananas are climacteric fruits and ripening is regulated by ethylene produced by the fruit and involves numerous biochemical changes including the conversion of starch to sugars, cell wall disassembly, synthesis of volatile compounds, changes in  
20 phenolic constituents and degradation of chlorophyll in the peel. The conversion of starch to sugars is particularly striking, where starch accounts for 20-25% of the fresh weight of the unripe fruit and depending on the genetic background, can be converted almost entirely to sugars.

The triploid nature of the cultivated dessert banana crop has hampered conventional methods  
25 of breeding for improved characteristics. As a result of this an enormous pool of genetic resources for enhancing postharvest characteristics of the fruit has remained untapped.

According to the present invention there is provided a method of modulating the ripening or tissue senescence process in plants of the genus *Musa* comprising inserting into plant  
30 material at least one polynucleotide sequence selected from the sequences depicted as SEQ ID-Nos. 1 -57, regenerating said plant material and selecting from the transformed

regenerants, plants with modulated ripening or tissue senescence characteristics. The said polynucleotide may be obtained from the cDNA library having the NCIMB Accession Number 40814.

Further according to the present invention is a method of modulating the ripening or tissue senescence process in plants of the genus *Musa* comprising inserting into plant material at least one polynucleotide sequence or a fragment thereof, obtainable by hybridisation, from the cDNA library having the NCIMB Accession Number 40814, by the use of at least one of the sequences depicted as SEQ ID Nos 1-57 as oligonucleotide probes, said hybridisation being conducted at a temperature from 60°C to 65°C in 0.3 strength citrate buffered saline containing 0.1% SDS followed by rinsing at the same temperature with 0.3 strength citrate buffered saline containing 0.1% SDS, regenerating said plant material and selecting from the transformed regenerants, plants with modulated ripening or tissue senescence characteristics. The invention further provides a method as described above wherein the said polynucleotide is capable of modulating the production of pectate lyase and more specifically the polynucleotide comprises at least one of the sequences depicted in the sequence listings as SEQ-ID-Nos. 13-18.

A preferred method for inserting the said polynucleotides into plant material according to the method of the present invention, may be selected from the group comprising the *Agrobacterium*, microparticle bombardment, fibre mediated or direct insertion methods.

The invention further provides plants, their progeny and seed and material obtained from said plants, produced according to the method of the present invention. It is preferred that the said plants, their progeny and seed and material obtained from said plants are derived from plants of the genus *Musa*.

The present invention also provides a vector functional in plants comprising a promoter region which is operable in plant cells, at least one of the polynucleotide sequences described above and a transcription termination sequence. The promoter may be constitutive, developmentally regulated or switchable. In addition to this the promoter may also be tissue specific or organ specific.

Further provided is a banana produced via the preceding method, having altered fruit characteristics when compared with a banana which is not transformed with at least one of the polynucleotide sequences described above.

The present invention also provides an improved method of controlling plant pathogens comprising the application of an anti-pathogenic agent to plants, characterised in that plants to which the said agent is applied, are plants according to the present invention.

The gene sequences of the present invention may be synthesised *ab initio*, using the sequence data in the sequence listing provided herewith, or isolated from a library using the standard techniques known within the art. The sequences depicted in the sequence listing or parts thereof may also be used to create oligonucleotide probes for the purposes of isolating from the library those polynucleotides which are capable of producing the desired proteins. To assist the isolation of these polynucleotides we have deposited with the National Collection of Industrial & Marine Bacteria, St. Machar Drive, Aberdeen, UK, a cDNA library of the banana peel ripening related genes. The library was deposited on 9th July 1996 and has the NCIMB Accession Number 40814.

Thus, this invention is based on the identification of genes which encode proteins involved in banana ripening-related processes, specifically within banana pulp. DNA sequences according to the sequence listing or those sequences obtainable from the deposited library, may be used in the process of modifying the plant ripening characteristics of plants and/or fruit.

By virtue of this invention banana plants can be generated which, amongst other phenotypic modifications, may have one or more of the following fruit characteristics: improved resistance to damage during harvest, packaging and transportation due to slowing of the ripening and over-ripening processes; longer shelf life and better storage characteristics due to reduced activity of degradative pathways (e.g. cell wall hydrolysis); improved processing characteristics due to changed activity of proteins/enzymes contributing to factors such as: viscosity, solids, pH, elasticity; improved flavour and aroma at the point of sale due to modification of the sugar/acid balance and other flavour and aroma components responsible for characteristics of the ripe fruit; modified colour due to changes in activity of enzymes involved in the pathways of pigment biosynthesis (e.g. lycopene,  $\beta$ -carotene, chalcones and anthocyanins); increased resistance to post-harvest pathogens such as fungi.

The activity of the ripening-related proteins may be either increased or reduced depending on the characteristics desired for the modified plant part (fruit, leaf, flower, etc). The levels of protein may be increased: for example, by incorporation of additional genes. The additional

genes may be designed to give either the same or different spatial and temporal patterns of expression in the fruit. "Antisense" or "partial sense" or other techniques may be used to reduce the expression of ripening-related protein.

The activity of each ripening-related protein or enzyme may be modified either individually  
5 or in combination with modification of the activity of one or more other ripening- related proteins/enzymes. In addition, the activities of the ripening-related proteins/enzymes may be modified in combination with modification of the activity of other enzymes involved in fruit ripening or related processes.

DNA constructs according to the invention for gene silencing, may comprise a base sequence  
10 at least 10 bases (preferably at least 35 bases) in length for transcription into RNA. There is no theoretical upper limit to the base sequence, it may be as long as the relevant mRNA produced by the cell but for convenience it will generally be found suitable to use sequences between 100 and 1000 bases in length. When using genomic DNA as the source of a base sequence for transcription it is possible to use either intron or exon regions or a combination  
15 of both.

As a source of the DNA base sequence for transcription, a suitable cDNA or genomic DNA or synthetic polynucleotide may be used. The isolation of suitable ripening-related sequences is described above; it is convenient to use DNA sequences derived from the ripening-related clones deposited at NCIMB in Aberdeen. Sequences coding for the whole,  
20 or substantially the whole, of the appropriate ripening-related protein may thus be obtained. Suitable lengths of this DNA sequence may be cut out for use by means of restriction enzymes. The preparation of such constructs is described in more detail below.

Constructs suitable for expression of the appropriate ripening-related sequence in banana cells, may be produced using a cDNA sequence selected from the deposited library having  
25 the NCIMB Accession Number 40814 or the gene sequence as found in the chromosome of the banana plant. Recombinant DNA constructs may be made using standard techniques.

In this specification modulation means an increase or decrease of the desired effect.

More specifically "modulation of the ripening or tissue senescence process in plants of the genus *Musa*" means an increase or decrease in production of a ripening related protein  
30 resulting from the method as described above. For example, where an increased ripening related protein is desired, plants may be transformed according to the method as described

above and those plants exhibiting the desired effect may be selected from the population of transformants. Furthermore, it may be desirable to provide a plant with modulated ripening or tissue senescence characteristics by increasing the production of one protein and decreasing the production of another protein in the same plant. For example, a banana fruit, modified using the present method, and having decreased levels of the enzyme pectate lyase would be beneficial because pulp softening would require a substantially longer time when compared with a control. In addition to this and by increasing the levels of another ripening related protein such as an antifungal protein in the same fruit using the present method, would complement the extended life of the banana pulp with increased resistance to disease.

10 Increase in production of a ripening related protein includes inserting into plant material one or more copies of any of the polynucleotides described above, wherein the said polynucleotides must be capable of producing a protein and thereby increasing protein levels when compared with a control plant.

Decrease in production of a ripening related protein includes inserting into plant material one or more copies of any of the polynucleotides described above, wherein the said polynucleotides must be capable of producing an mRNA which is capable of interfering with endogenous mRNA to such a degree that the levels of translated protein are reduced when compared with a control plant.

Ripening process of plants means the process of maturing or developing .

20 Senescence means the progressive deterioration in function of cells, tissues, organs etc., related to the period of time since that function commenced..

Control plant means a comparable plant used for the purposes of determining modulation of the ripening or tissue senescence process effect in plants. Specifically, in plant transformations the control plant is usually of the same species and variety as the material used before the transformation process and is grown in the same conditions, (usually with the transformant selection step modified in some way on the part of the control plant), as the transformed plants. More specifically the control plant may comprise an untransformed control plant or a transformed control plant providing it has not already been transformed with the same polynucleotide sequence as the plant material to be transformed.

30 "Plant material" includes plant cells and any other type of plant regenerable material.



The following examples further illustrate the invention but are not to be construed to limit the scope thereof:

TABLE 1. Is a list of clones isolated from banana pulp and the corresponding sequence identity number as provided in the sequence listing herein. The table also illustrates the approximate clone size, the percentage identity and, where relevant, nucleotide similarity with published sequences, based on the results obtained from comparisons with the EMBL sequence database. The table also provides, where relevant, the gene identity of those published sequences and their database accession numbers.

FIGURE 1. Plant transformation vector pUN, containing the UBI polyubiquitin promoter.

FIGURE 2. Plant transformation vector pSHYN, containing hygromycin resistance gene for selection of transformed plants.

FIGURE 3. Plant transformation vector pAN, containing the banana ACC oxidase promoter.

#### EXAMPLE 1

##### Construction of a cDNA library of ripening genes

###### 1.1 Isolation of messenger RNA

Total RNA was isolated from ripening (24 hours after ethylene treatment) banana pulp (*Musa acuminata* cv. Grand Nain) as described by Chang et al, Plant Molecular Biology Reporter, Vol. 11(2) 113-116 (1993). Messenger RNA was isolated from total RNA by Oligo(dT)-cellulose chromatography according to Bantle et al., Analytical Biochemistry 72, 413-427 (1976).

###### 1.2 Synthesis of cDNA and Cloning into Vector

The first and second strands of the cDNAs were synthesised from the messenger RNAs using a commercial cDNA synthesis kit (Catalog No. 200450, ZAP Express™ Gold Cloning kit, Stratagene Ltd, Cambridge, Cambs, UK). Double stranded cDNAs were cloned into the ZAP Express™ vector, packaged, mixed with plating bacteria to determine titre and for library screening, following instructions of the suppliers protocol.

### 1.3 Screening of the cDNA library from banana pulp.

The unamplified cDNA library from ripening banana pulp was differentially screened using cDNA from unripe and ripening banana peel tissue. A proportion of the library was plated individually at low density and duplicate plaque lifts made onto Hybond N nylon filters (Amersham) according to the manufacturer's instructions. One filter was hybridised to dCTP radiolabelled cDNA from green fruit and the duplicate filter hybridised to dCTP radiolabelled cDNA from ripening fruit. Hybridization's were at high stringency. Plaques hybridising preferentially with ripening or green radiolabelled cDNA were picked and re-plated for a second round of selection by differential screening. These clones were numbered as ripening up- or down-regulated peel clones. The clones were in-vivo excised from the ZAP express™ vector into the pBK-CMV phagemid vector using the ExAssist™ interference-resistant helper phage, following instructions from manufacturers protocol.

### 1.4 Characterisation of the ripening pulp cDNA library and the ripening-related clones.

The ripening cDNA library from pulp tissue were prepared with an efficiency of  $3.2 \times 10^5$  plaque-forming units per microgram of cDNA. The sizes of the inserts in the peel library was 0.4 - 6.7 Kb with a mean size insert of 1.47 Kb.

From the 250 plaques used in the first screen, 73 putative ripening-related clones were obtained. These 73 clones were partially sequenced using the ABI PRISMTM Dye Terminator Cycle Sequencing Ready Reaction kit with AmpliTaq® DNA polymerase (Applied Biosystems, Warrington, Cheshire, UK) with forward primers specific for the pBK-CMV vector. From these, the following ripening-related clones were selected. Comparisons of these sequences in the EMBL database using GCG ('Wisconsin') software has identified homologies for the clones listed in TABLE 1 below.

## EXAMPLE 2

Construction of truncated sense RNA vectors with the maize polyubiquitin promoter.

A vector is constructed using the sequences corresponding to a fragment of the inserts of one of the sequences 1 to 57. This fragment is synthesised by polymerase chain reaction using synthetic primers incorporating BamHI restriction sites suitable for cloning between a

maize UBI polyubiquitin promoter (Christensen et al, 1992, Plant Molecular Biology, 18:675-689) and a nopaline synthase 3' end termination sequences in the vector pUN (Fig. 1.).

The truncated sense expression cassette is excised by digestion with *AscI*, the ends of the fragment are made flush with T4 polymerase and it is cloned into the vector pSHYN (Fig. 2.) which has been cut with *KpnI* and the ends made flush with Klenow polymerase. pSHYN contains hygromycin resistance gene for selection of transformed plants.

After synthesis of the vector, the structure and orientation of the sequences are confirmed by DNA sequence analysis.

### EXAMPLE 3

Construction of truncated sense RNA vectors with a fruit enhanced promoter.

The 1386bp *HindIII* fragment containing the banana ACC oxidase promoter (UK.

Application No. 9607700.3) is cloned the *HindIII* site in pMSC2 (Fig. 3.) to give the vector pAN.

A vector is constructed using the sequences corresponding to a fragment of the inserts of one of the sequences 1 to 57. This fragment is synthesised by polymerase chain reaction using synthetic primers incorporating *BamHI* restriction sites suitable for cloning between a maize UBI polyubiquitin promoter (Christensen et al, 1992, Plant Molecular Biology, 18:675-689) and a nopaline synthase 3' end termination sequences in the vector pAN.

The truncated sense expression cassette is excised by digestion with *AscI*, the ends of the fragment are made flush with T4 polymerase and it is cloned into the vector pSHYN (Fig. 2.) which has been cut with *KpnI* and the ends made flush with Klenow polymerase. pSHYN contains hygromycin resistance gene for selection of transformed plants.

After synthesis of the vector, the structure and orientation of the sequences are confirmed by DNA sequence analysis.

### EXAMPLE 4

Construction of an over-expression vector with the maize polyubiquitin promoter.

The complete sequence of a ripening -related cDNA containing a full open-reading frame is inserted into the vectors described in EXAMPLE 2.

#### EXAMPLE 5

5

Construction of an over-expression vector with a fruit enhanced promoter.

The complete sequence of a ripening -related cDNA containing a full open-reading frame is inserted into the vectors described in EXAMPLE 3.

10

#### EXAMPLE 6

Generation of transformed Musa plants

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Transformed Musa plants containing the vectors are produced by the method described in Sagi et al. (1995) Biotechnology. Vol. 13 pp 481-485. Regenerated transformed plants are identified by their ability to grow on hygromycin and grown to maturity. Ripening fruit are analysed for a modulation in their ripening related or senescence characteristics.

20

Other suitable transformation methods for banana are described in Sagi et al. (1994) Plant Cell Reports. Vol. 13. pp 262-266. and May et al. (1995) Biotechnology. Vol. 13 pp 486-492.

TABLE I

Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ-ID-NO-1	Pulp Upregulated	U-U9	1	Isoflavone Reductase	61.6	714	Potato ( <i>Solanum tuberosum</i> ), X92075
SEQ-ID-NO-2	Pulp Upregulated	U-U17	1	Isoflavone Reductase	62.9	770	Potato ( <i>Solanum tuberosum</i> ), X92075
SEQ-ID-NO-3	Pulp Upregulated	U-U66	1.1	Isoflavonoid Reductase	60.0	722	<i>Arabidopsis thaliana</i> , Z49777
SEQ-ID-NO-4	Pulp Upregulated	U-U104	1	Isoflavonoid Reductase	60.6	696	<i>Arabidopsis thaliana</i> , Z49777
SEQ-ID-NO-5	Pulp Upregulated	U-U13	1.1	Beta-1,3-Glucanase	58.5	585	Soybean ( <i>Glycine max</i> ), A26451
SEQ-ID-NO-6	Pulp Upregulated	U-U136	1.3	Beta-1,3-Glucanase	59.8	800	Barley ( <i>Hordeum vulgare</i> ), M91814
SEQ-ID-NO-7	Pulp Upregulated	U-U21	1.8	Transcriptional Activator	54.3	311	<i>Zea mays</i> , L13454

Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ-ID-NO-8	Pulp Upregulated	U-U31	0.55	S-adenosylhomocysteine Hydrolase	67.0	467	Orchid ( <i>Phalaenopsis sp.</i> ), X79905
SEQ-ID-NO-9	Pulp Upregulated	U-U131	1.8	S-adenosyl L-homocysteine Hydrolase	79.8	699	Wheat ( <i>Triticum aestivum</i> ), L11872
SEQ-ID-NO-10	Pulp Upregulated	U-U32	0.8	Beta-amylase	54.7	854	<i>Zea mays</i> , Z25871
SEQ-ID-NO-11	Pulp Upregulated	U-U55	0.8	O-methyl transferases	60.1	223	<i>Zea mays</i> , L14063
SEQ-ID-NO-12	Pulp Upregulated	U-U72	0.8	O-methyl transferase	60.6	226	<i>Zea mays</i> , L14063
SEQ-ID-NO-13	Pulp Upregulated	U-U68	1.8	Pectate Lyase	57.9	394	<i>Lilium longiflorum</i> , Z17328
SEQ-ID-NO-14	Pulp Upregulated	U-U69	1.7	Pectate Lyase	66.1	516	<i>Zea mays</i> , L20140
SEQ-ID-NO-15	Pulp Upregulated	U-U84	1.1	Pectate Lyase	65.8	736	<i>Lycopersicon esculentum</i> , X55193
SEQ-ID-NO-16	Pulp Upregulated	U-U89	1.6	Pectate Lyase	54.8	354	<i>Nicotiana tabacum</i> , X67158

- 13 -

Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-17	Pulp Upregulated	U-U115	1.5	Pectate Lyase	67.3	508	<i>Zea mays</i> , L20140
SEQ -ID-NO-18	Pulp Upregulated	U-U117	1.7	Pectate Lyase	55.0	333	<i>Lilium longiflorum</i> , Z17328
SEQ -ID-NO-19	Pulp Upregulated	U-U80	0.6	Vicilin-like storage protein	53.7	387	<i>Arabidopsis thaliana</i> , T13642
SEQ -ID-NO-20	Pulp Upregulated	U-U90	1.8	Glutamate Decarboxylase	72.5	735	<i>Petunia hybrida</i> , L16797
SEQ -ID-NO-21	Pulp Upregulated	U-U92	1.8	Glutamate Decarboxylase	71.8	740	<i>Arabidopsis thaliana</i> , U10034
SEQ -ID-NO-22	Pulp Upregulated	U-U91	1.1	Aconitase	76.4	766	Pumpkin ( <i>Cucurbita sp.</i> ), D29629
SEQ -ID-NO-23	Pulp Upregulated	U-U96	0.9	Express Sequence Tag.	69.0	452	<i>Arabidopsis thaliana</i> , H36910
SEQ -ID-NO-24	Pulp Upregulated	U-U103	2	Cell Wall Invertase	66.0	567	<i>Zea mays</i> , U17695
SEQ -ID-NO-25	Pulp Upregulated	U-U93	3.5	Heat Shock Protein cognate	76.4	711	<i>Lycopersicon esculentum</i> , X54030
SEQ -ID-NO-26	Pulp Upregulated	U-U125	1.8	Heat Shock Protein	71.0	662	<i>Spinacia oleracea</i> , L26243
SEQ -ID-NO-27	Pulp Upregulated	U-U105	0.9	Hexa ubiquitin Protein	64.1	237	Sunflower ( <i>Helianthus annuus</i> ), X57004

Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ-ID-NO-28	Pulp Upregulated	U-U116	0.8	Polyubiquitin	81.0	625	Rice ( <i>Oryza sativa</i> ), X76064
SEQ-ID-NO-29	Pulp Upregulated	U-U120	0.9	Extensin	56.9	576	Almond ( <i>Prunus amygdalus</i> ), X65718
SEQ-ID-NO-30	Pulp Upregulated	U-U126	1.2	Basic Chitinase	63.2	506	Cowpea ( <i>Vigna unguiculata</i> ), X88801
SEQ-ID-NO-31	Pulp Upregulated	U-U129	1.3	Beta-glucosidase	60.9	517	White clover ( <i>Trifolium repens</i> ), X56733
SEQ-ID-NO-32	Pulp Upregulated	U-U130	1.3	Chlorophyll a/b binding protein	52.0	415	Rice ( <i>Oryza sativa</i> ), D00641
SEQ-ID-NO-33	Pulp Upregulated	U-U43	2.5	Fruit sp pp involved in maturation	53.8	396	Tomato ( <i>Lycopersicon esculentum</i> ), X13743
SEQ-ID-NO-34	Pulp Upregulated	U-U70	0.6	Root specific protein	63.6	420	Rice ( <i>Oryza sativa</i> ), L27208
SEQ-ID-NO-35	Pulp Upregulated	U-U16	0.6	-	-	-	No published sequence similarity
SEQ-ID-NO-36	Pulp Upregulated	U-U30	0.8	-	-	-	-
SEQ-ID-NO-37	Pulp Upregulated	U-U40	1.0	-	-	-	-
SEQ-ID-NO-38	Pulp Upregulated	U-U108	1.1	-	-	-	-



Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-39	Pulp Upregulated	U-U128	2.2	-	-	-	-
SEQ -ID-NO-40	Pulp Down regulated	U-D4	1.3	Granule Bond Starch Synthase	62.3	621	Cassava ( <i>Manihot esculenta</i> ), X74160
SEQ -ID-NO-41	Pulp Down regulated	U-D10	1.3	Starch Synthase	68.8	506	Pea ( <i>Pisum sativum</i> ), X88789
SEQ -ID-NO-42	Pulp Down regulated	U-D13	1.3	Starch Synthase	67.4	454	Pea ( <i>Pisum sativum</i> ), X88789
SEQ -ID-NO-43	Pulp Down regulated	U-D66	1.3	Granule Bond Starch Synthase	64.1	669	Cassava ( <i>Manihot esculenta</i> ), X74160
SEQ -ID-NO-44	Pulp Down regulated	U-D111	1.3	Starch Synthase	66.4	655	Cassava ( <i>Manihot esculenta</i> ), X74160
SEQ -ID-NO-45	Pulp Down regulated	U-D112	2.3	Granule Bond Starch Synthase	68.4	196	Potato ( <i>Solanum tuberosum</i> ), X58453

Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ-ID-NO-46	Pulp Down regulated	U-D39	1.1	Antifungal Protein	69.1	517	<i>Zea mays</i> , U06831
SEQ-ID-NO-47	Pulp Down regulated	U-D50	1.3	Basic Chitinase	60.2	678	<i>Cowpea (Vigna unguiculata)</i> , X88801
SEQ-ID-NO-48	Pulp Down regulated	U-D86	1.7	Basic Chitinase	63	578	<i>Cowpea (Vigna unguiculata)</i> , X88801
SEQ-ID-NO-49	Pulp Down regulated	U-D90	1.3	Basic Chitinase	61.8	670	<i>Cowpea (Vigna unguiculata)</i> , X88801
SEQ-ID-NO-50	Pulp Down regulated	U-D93	0.7	Basic Chitinase	61.6	701	<i>Cowpea (Vigna unguiculata)</i> , X88801
SEQ-ID-NO-51	Pulp Down regulated	U-D61	1	Beta-glucanase	61.9	795	Barley ( <i>Hordeum vulgare</i> ), X52572
SEQ-ID-NO-52	Pulp Down regulated	U-D63	2.3	Nodulin Gene	50.4	637	Lucerne ( <i>Medicago sativa</i> ), X13287

-17-

Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ-ID-NO-53	Pulp Down regulated	U-D65	0.9	Extensin	56.7	556	Cowpea ( <i>Vigna unguiculata</i> ), X91836
SEQ-ID-NO-54	Pulp Down regulated	U-D84	0.8	Extensin	58.3	492	Cowpea ( <i>Vigna unguiculata</i> ), X91836
SEQ-ID-NO-55	Pulp Down regulated	U-D75	1.2	Wali 7	74.4	703	Wheat ( <i>Triticum aestivum</i> ), L28008
SEQ-ID-NO-56	Pulp Down regulated	U-D83	1.2	Wali 7	72.8	743	Wheat ( <i>Triticum aestivum</i> ), L28008
SEQ-ID-NO-57	Pulp Down regulated	U-D64	2.3	-	-	-	-

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

(A) NAME: ZENECA LIMITED  
(B) STREET: 15 STANHOPE GATE  
(C) CITY: LONDON  
(D) STATE: LONDON  
(E) COUNTRY: UNITED KINGDOM  
(F) POSTAL CODE (ZIP): W1Y 6LN

(ii) TITLE OF INVENTION: GENETIC CONTROL OF FRUIT RIPENING

(iii) NUMBER OF SEQUENCES: 57

## (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## (v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: GB PPD

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 785 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

## (vii) IMMEDIATE SOURCE:

(B) CLONE: U-U9

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

45	CGGCACGAGG AAAA ACTANG TGAGAANGAG ATAATCGTTG ACCGAGGNAG AGAATGGCGA	60
	GCGAGAAGAG CAAATCCTG ATCATCGGGG GCACCGGGTA CATCGGCAAG TTCATCGTGT	120
50	TTGCGAGCGC CAGGTTAGGT AACCTACCT TCGCTCTCGT CCGGAGCACC ACCGCCCCCG	180
	CCGGCCAACC CGAGAAGGCC AAGCTCTGA GCGACTTCCA GGCCGCCGGC GTCACCCTCG	240
	TCCAGGGGGA TATNTATAAC CACGAGAGTC TGGTTAAGGC GATCAAGCTG GTGGATGTGG	300
55	TCATCTCCCC CGTCGGCTTC GGGCANCTGA NTGATCAGAC CAAGATCATC GACGCCATCN	360
	AANAAGCCGG AGGACACATC AAGAGGTACC TTCCATCGGA GTTTGGCAAC GACGTANACC	420
60	GAAGCCATGC TGTGGAGCCA GCAAAGTCTA CCTTTGTCGT CAAGCAACAA ATCANAAGGG	480
	CTGTTGAGGC ATCGGGTNTC CTTACACCT TTGTATCTTC CAACTTTCTT CGGTGGGTNT	540
	TTCTCCCCG TATTATGACA GGCAGGAGCC ACTGGTCCTC CCACGGACAA GGTGTGCATC	600
65	TTAGGTNACG GGAACNCAA ACGATCTTCT CNATGAANAC GACTTCCGGA CATCCCATT	660
	ANTCTTGAT GATCCATAAC CTGAACCAGG TTCTATTTCT TAAACTTCC NCCACTTCTT	720
70	NTCTCTTANC ANCTCNTTTC CCTCTTGGGA AAAAAATGTC NNCTANACTT CNAAGGGT	780
	TTANT	785

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: U-U17

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

20	CGCGCACGAG GAAGAAACT AGGTGAGAAN GAGATAATCG TTGACCGAGG NAGAGAATGG	60
	CGAGCGAGAA GAGCAAATC CTGATCATCG GGGGCACCGG GTACATCGGC AAGTTCATCG	120
	TGTTTTCGAG CGCCAGGTTA GGTAACCTA CCTTCGCTCT CGTCCGAGC ACCACCGCCC	180
25	CCGCCGGCCA ACCCGAGAAG GCCAAGCTCC TGAGCGACTT CCAGGCCGCC GCGGTCACCC	240
	TCGTCCAGGG GGATATATAT AACCACGAGA GTCTGGTTAA GGCGATCAAG CTGGTGGATG	300
30	TGGTCATCTC CCCCCTCGGC TTCGGGCANC TGANTGATCA GACCAAGATC ATCGACGCCA	360
	TCAAAGAAGC CGGAGGACAC ATCAAGAGGT ACCTTCCATC GGAGTTTGGC AACGACGTAN	420
35	ACCGAAGCCA TGCTGTGGAG CCAGCAAAGT CGACCTTTGT CGTCAAGCAA CAAATCANAA	480
	GGGCTGTTGA GGCATCGGGT ATCCCTTACA CCTTTGTATC TTCCAAC TTCGGTGGGT	540
	NTTTCCTCCC GGTATTANGA CAGGCAGGAG CCACTGGTCC TCCCACGGAC AAGGTTGTCA	600
40	TCTTANGTGA CGGGAACACA AAAGCGATCT TTCTCAATGA ANACACATCC GGACNTNCAC	660
	NATTAAAGCA GTGGATGATC CGAAAACCTG AACANGTTCT ATATCTGAAA CCTTCCGCCA	720
45	CTCTTGCTCT ATNACAACTC ATTTCCCTCT GGGAAAAAAA NGTCNGCAAA ACTCCNAAAA	780
	GGTCTACTTC CCGGAAGAAA AATCTGAANC ANA	813

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: U-U66

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

65	GGCACGAGGG GAAAAGGAGA TNATCGTTGA CCGAGGAGAG AATGGCGAGC GAGAAGAGCA	60
	AGATCCTGAT CATCGGGGGC ACGGGGTACA TCGGCAAGTT CATCGTGTTC GCGAGCGCCA	120
70	GGTTAGGTAA CCCTACCTTC GCTCTCGTCC GGAGCACCAC CGCCCCGCC GGCCAACCCG	180

AGAAGGGCAA GCTCCTGAGC GACTTCCAGG CCGCCGGCGT CACCCTGGTC CAGGGGGATA 240  
 TATATAACCA CNAGAGTCTG GTTAAGGCGA TCAAGCTGGT GGATGTGGTC ATCTCCCCCG 300  
 5 TCGGCTTCGG GCAGCTGAGT GATCAGACTA AGATCATCGA CGCCATCAAA GAAAGCCGGA 360  
 GGACACATCA AGAGGTACCT TCCATCGGGA GTTTGGCAAC GACGTANACC GAAGCCATGC 420  
 10 TGTGGAAGCC ANCAAAGTCG ACCTTTGTCTG TCAAGCAACA AATTANAAGG GCTGTTGAGG 480  
 CATCGGGGAT CCCTTACACC TTTGTTATCT TCCAATTCT TCGGTGGGTA TNTCCTCCCC 540  
 GTATTGGGAC AGGCANGAAC CACTGGTCCT CCCACGGAC AAGGTTGTCTN TCTTAGGTGA 600  
 15 ACGGGAACAC CAANGCGATC TTTCTCAATG AAAGACAAC TCGGACATNC CCNATTTAAC 660  
 CANTGGATGA TCCNANAACC TGAACAAGGT CTATTTCTGA AAACCTTCNC ATCTTCTTTT 720  
 TCTCATAACG AACCCNTTTN CCTCTT 746  
 20

## (2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 795 base pairs  
 25 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA  
 30

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U104  
 35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGCACGAGGA AANGAGATAA TCGTTGACCG AGGCAGAGAA TGGCGAGCGA GAAGAGCAAA 60  
 40 ATCTGATCA TCGGGGGCAC CGGGTACATC GGCAAGTTCA TCGTGTTCG GAGCGCCAGG 120  
 TTAGGTAACC CTACCTTCGC TCTCGTCCGG AGCACCACCG CCCCCGCCGG CCAACCCGAG 180  
 45 AAGGCCAAGC TCCTGAGCGA CTTCCAGGCC GCCGGCGTCA CCCTCGTCCA GGGGGATATA 240  
 TATAACCACG AGAGTCTGGT TAAGGCGATC AAGCTGGTGG ATGTGGTCAT CTCCCCGTC 300  
 GGCTTCGGGC AGCTGAGTGA TCAGACCAAG ATCATCGACG CCATCAAAGA AGCCGAGGA 360  
 50 CACATCAAGA GGTACCTTCC ATCGGGAGTT TGGCAACGAC GTTANACCGA AGCCATGCTG 420  
 TGGAGCCAGC AAAGTCNACC TTTGTCTGCA AGCAACAAAT CANAAGGGCT GTTGANGCAT 480  
 55 CGGGTNTCCC TTACACCTTT GTATCTTCCA ACTTCTTCGG TGGGTATTTT CTCCCGGTAT 540  
 TANGACAGGC AGGACCACTG GTCCTCCCCA CNGACAAGGT TGTCTCTTA GGTGACNGGA 600  
 ACACAAAANC ATCTTTCTCN ATGAAGACAA CTCCGGACAT ACNCNATTAA AGCNGTGGAT 660  
 60 GATCCCAAAA CCTGAACAAG TTCCTATNTC TTGAAAACCT TCCCGCCCAA CCATCCTTTN 720  
 GTTCTCCNT TAAACCNAAC CTCCATTTTC CCCTCCTTGG GGAAAAAAA AAGGTCCGGC 780  
 65 NAANAACCTC CNAAA 795

## (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 797 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: cDNA

10

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-U13

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CGGCACGAGG NAGAACCTTT TGACAGAGTT GTTGTATGG CAACAAAAGC TTCTCTCTCC 60  
ATAAAAGGCT TTGCCTTGCT GGTTCAGTC CTTGTAGCAG TTCCAACAAG AGTGCAATCG 120  
20 ATTGGTGTCT GCTACGGCAT GCTCGGCAAC AATCTTCCCC CGCCAGCGA GGTGGTCAGT 180  
CTCTACAAAT CCAACAACAT CGCGAGGATG AGACTCTACG ATCCAAACCA AGCCGCCCTG 240  
CAAGCCCTCA GGAAGTCCAA CATCCAAGTC CTGTTGGATG TCCCCGATC CGACGTGCAG 300  
25 TCACTGGCCT CCAATCCTTC GGCCGCCGGC GACTGGATCC GGAGGAACGT CGTCGCCTAC 360  
TGGCCAGCG TCTCCTTTCG ATACATAGCT GTCGAAACG AGCTGATCCC CGGATCGGAT 420  
30 CTGGCGCAGT ACATCCTCCC CGCCATGCGC AACATCTACA ATGCTTTGTC CTCGGCTGGC 480  
CTGCAAAACC AGATCAAGGT CTCGACCGCG GTCGACACGG GCGTCCTCGG CACGTCCTAC 540  
CCTCCCTCCG CCGGCGCCTT CTCCTCCGCC GCCAGGCGT TACCTGANCC CCATCGTGCA 600  
35 GTTCTTGGCG ANTAACGGAA CGCCGCTCCT GGTCAATGTG TACCTTATTT TAACTACACC 660  
GGCAACCCGG GANAGATCTC GCTGCCTACN CCCTGTTAC GGCCNCGGGG TCTCNTGCAG 720  
40 GATGGGCGAA TTCNCTATC ANAANTGTT CANTCCATCT TCNAAACCGG TCTTCCCGGG 780  
CTGGAAAAAA TTGGAAG 797

45

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 792 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

50

(ii) MOLECULE TYPE: cDNA

55

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-U136

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGCAGGAGGA GAACCTTTTT GACAGAGTTG TTGTCATGGC AACAAAAGCT TCTCTCTCCA 60  
TAAAGGCTT TGCCTTGCTG GTTTCAGTCC TTGTAGCAGT TCCAACAAGA GTGCAATCGA 120  
65 TTGGTGTCTG CTACGGAATG CTCGGCAACA ATCTTCCCCC GCCAGCGAG GTGGTCAGTC 180  
TCTACAAATC CAACAACATC GCGAGGATGA GACTCTACGA TCCAAACCAG GCCGCCCTGC 240  
70 AAGCCCTCAG GAACTCCAAC ATCCAAGTCC TGTGGATGT CCCCCGATCC GACGTGCAGT 300

CACTGGCCTC CAATCCTTCG GCCGCCGGCG ACTGGATCCG GAGGGAACGT CGTCGCCTAC 360  
 TGGCCCAGCG TCTCCTTTTCG ATACATAGCT GTCGGAAACG ANCTGATCCC CGGATCGGAT 420  
 5 CTGGCGCAGT ACATCCTCCC CGCCATGCGC AACATCTACA ATGCTTTGTC CTCGGCTGGC 480  
 CTGCAAAACC AGATCAAGGT CTCCGACCGC GGTGACACG GCGTCCTCG GCACGTCCTA 540  
 10 CCCTCCCTCC CGCCGGNGCC TTCTCCTCCG CCGCCCAAGC GTNCTGANCC CCATCGTGCA 600  
 NTTCTTTGGC GAAATAACGG ANCGCCGCTC CCNGGTCCAT GTTTTCCCT TATTTTAACT 660  
 ACNCCGGCAA CCCNGGAAAG ATTTGCTGC CCTTACGCC CCTGGTTTCC NNGGGGCTTC 720  
 15 CCGGGCGTTT CTTCCTTTGC CAGGGANTNG GGGCGAATTC CCNNCTTTTC CANAAACCTT 780  
 GTTCCAACNC CC 792

## (2) INFORMATION FOR SEQ ID NO: 7:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 855 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown  
 (ii) MOLECULE TYPE: cDNA

30 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U21

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CGGCACGAGT CTCTCTCTGT CTCTCCGTCG TCTCGTTGTC TGTTCTTAG GGCTTGCGAT 60  
 CGCCACCGGT CGCGAGGGTT GGAGCCATGG AATTCTTGCG GTTTGGGGCT GAGGTGGCGG 120  
 40 CAGGAGAGGA AGCCGCGACG GGGTACTGGA TGCGATGGCA GACGCTCGTC TCGCTCTGA 180  
 TCGTCGTCGC CCCGGCGGTC GCCGCGGTGG TTGTCGCGGC GCGGGCGCCG GCGCCGGCGC 240  
 45 GACCGCTCAG GGCCGTCGAT CTCTGGGCGC CGTGCTGGGC CGGGATGCAC CCGGCCTGGC 300  
 TTCTCGCGTA CCGCGGCTTC NTGTTCTTGG CCATGCGGTG GCTACTCTTC CANATGATTC 360  
 TGTTTCGCGG ATTCTCCGCG TTCTACTTCT ATACTCAGTG GACGTTTGCC TTAGTCATTG 420  
 50 TCTATTTTGC GATCGCAACC ATTATATCCG CCCATGGCTG CTGGCTTTAC TCAAAGAGAA 480  
 GTATTATGCC AGATCAGGAG GTCAACAGAT TCCTAAATGG TGGTTTGTAG CANAATAGTC 540  
 55 CTATGACTCT ACCTTTGAGG ACCAACAAAA ATATGAATGT TATAAGATTG CAAAGCTATC 600  
 NTGAACAGGA NGCTGATGAA NAAAAANCTG GATTTTGGGG TCCTGCTATG CNACTNGTCT 660  
 ATCAAAACCA TTGCANGTGC TGTAATTGTT GAAANACATT GTATTTTGGG NTCNTNCTAA 720  
 60 TACCATATTT GTCTTCTATA AATTTAGGC TAAATGCTAT AATGGGCTGC ATGCATTCTC 780  
 TTAATGCTGT GTTTCTTCTA ATCCAACACT TTTCTCAATA ACCTGCCATT CCCNTNTTTC 840  
 65 NAATGSCATT TTGCG 855

## (2) INFORMATION FOR SEQ ID NO: 8:

70 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 722 base pairs  
 (B) TYPE: nucleic acid



(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-U31

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

15	CGGCACGAGA GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA	60
	GAGAGAGAGC CTAGACCGGC ATCNTCGTGC TTGCCGAGGG GCGGCTTATG ANTCTTGGTT	120
	GTGCCACTGG GCATCCAGC TTCGTCTGT CCTGCTCCTT CACCANCCAN GTGATNGCAC	180
20	NACTGGANTT ATGGANGGAA ANGGCGACCG GCNNGTACGA NAAGAANGTC TATGTGCTGC	240
	CCANGCNTCT GGATGAGAGG GTGGCNGCGC TCCNCTCGG CAAGCTGGGT GCCNCGCTCA	300
	CCNAGCTTAC NCCNTCGCGG GCTGATTACA TTAGCGTCCC GATCGAGGGA CCCTACANGC	360
25	CTGCTCACTA CNGGTATTNG GGTGCTTNT GCNAGAGACG ATGATNATAN NTCGGAGCAC	420
	TGGCNTTTTC GACTANNAGT TTGACCGATG GCTATGTTTCG TTTTGCTTTT CACCTTTTGT	480
30	CTTCCCATCT TTGCTGGTTC ACCTATGGAC GTTGTGTTCCA TTTGGATGTN NTGAGAAATG	540
	CTGATGGCAT TTTCGGAAAN AAAAANATNT AAAATCNCGA GAGTTCTTCT ANAGCGGCCG	600
	CGGGCCCNCT NNTTTTCCCC CGGGTGGGGT ACCANGTTG TGTNCCCNT TCCCCCTNTT	660
35	TGAGTCCTTT TACTNCCCCT GGCCGTCGTT TTATACNTCG TTGACTGGGA ANACCCTGCC	720
	NT	722

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 793 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-U131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

	GGCACGAGCC TTGCCCAACT CCTTCGATTC GTTCCAACGA TCGGAGAATG GCGCTGCTGG	60
60	TGGAGAANAC GTCGACGGGA CGCGAGTACA AGGTGAAGGA CCTTTCTCAG GCTGACTTCG	120
	GCCGCTCGA GATCGAGCTG GCGGAGGTGG AGATGCCGGG CCTCATGGCG TGCCGCGCCG	180
65	AGTTCGGGCC CGCCAAACCT TTCGCCGGCG CCCGCATCTC CGGCTCCCTC CACATGACCA	240
	TCCAGACCGC CGTCCTCATC GAGACCTCA CCGCCCTCGG TGCTGAAGTC CGGTGGTGCT	300
	CCTGCAACAT CTTCTCCACC CAGGACCACG CCGCTGCCGC CATTGCCCCG GACTCCGCCG	360
70	CCGTCTTCGC CTGGAAGGGA GAGACCTCG CCGAGTACTG GTGGTGACCC GAGCSATGCC	420

TCGACTGGGG CCCCAACGGT GGCCCCGACC TCATCGTCGA CAAAGGGGGT GACGCCACTC 480  
 TCCTCATCCA CGAAGGCGTC AAGGCTGANG AAGANTACGA AAAAGACCGG CAAGCTGCCC 540  
 5 GATCCGGCCT CCACGGAAAA CGCCGAATTC CAAATCGTGC TGGGGATTAT CCGCNANCGG 600  
 CTCCAGGTCN AACCCCNAAA ATTACCGCCC AGATNAAAGA ACCCTCCTCC GCTTTTTGAA 660  
 10 GAAAACANCN CTGGCGTTCA NCGAATCTAC CANATGCCAG GGCCANCNGG GGCCCCCTTG 720  
 TTCTTTCCCC CCNCCCANTC NAACNTTCN ACGAATCCCC GTTTTACCCN AAAAACCAAN 780  
 TTTTGAACAA CCT 793

15 (2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 847 base pairs  
 20 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

25

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U32

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CGGCACGAGG CGACGCCGGC CTTCGCCTCC GCGTCTCCCT CCACCTCCAC TGCCACCGCC 60  
 35 GCCCTCGCCT CCCCCTCCCC AAATCGGTCTG ACTCCGCCGC CGCTACAGAC CCCGACATCC 120  
 TATTCACTGA CCGCGCCGGC CGCCGCCGTG CCGACTGCCT CTCCTTCGCT GTCGACGACC 180  
 40 TCCCTGTCCT CGACGGCAGG ACCCCGATGG AAGCCTACGA GGAGTTCTTC CGGAGCTTCC 240  
 GCCTCGCCTT CGCTGACTTC TTTGGTTCCG TCATTACGGA TATCAGGATC GGTCTCGGGC 300  
 CAAATGGCGA GCTCCGTTAC CCTTCGTTTC CTCCCACTGG AAGCAATCGT TTCACCGGTG 360  
 45 TAGGAGAATT CCAGTGTTAT GACAAATACA TGCTTGCCGA TCTCAAACGA CACGCGGAGG 420  
 AAACCGGCAG CCCATTATGG GGCCTCTCTG GTCCTCACGA TGCCCCTGGG TACAACCACT 480  
 CTCCGGACTT CGGCAACTTT TTCAAGGACC ATGGCGGCTC CTGGGANACA CCCTACGGGC 540  
 50 AATTCTTCCT CTCCTGGTAC ACCGGCAAGC TCCTGTCTCA CGGTGACGGC CTGCTCTCGG 600  
 TCGCGTCAGA AGTATTGGTG ATTTGCCTGT CGCGCTCTCG GGCAAGGTTT CACTTTCTGC 660  
 55 ATTTGTTGGC AACGAACTC GGTGCGGCCC GTCTTANCTT GAAGGCCGGG TTCTNTNACA 720  
 CTTGACGGNA NAANAACNGG TTTCAAGGAT GTTGGCTAAN ATCTCCCGAA ANCNTCCTGC 780  
 60 ANCATGATTC ATCCCGGGCN TGGACTTCTC NGAAGGGGAA CANTCCTCAG GGTGTTCCGG 840  
 TCTGCCC 847

(2) INFORMATION FOR SEQ ID NO: 11:

65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 822 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 70 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-U55

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

10	GGCACGAGGC ATGGAGAACC CTGTTGCGAT GGGCATCATG GAGGAGCTTG AGGCCCAGAG	60
	CGAGGTGTGG AACCACATTT TTAGATTCAT CACCTCCATG TCCGTCAAGT GCGCGGTGGA	120
	GCTCAGGGTC CCCGACGCCA TCCACGCCCA CGGCGGCAAC GCAACTCTCC CTCAGCTGGC	180
15	CGCCGCCCTC AGCCTCCCTC CCGCCAAGCT CGCCGACCTC CGACGCCTCA TGCGCATGCT	240
	GGTCCACGCC GGCTGCTTCG CCAAGCAGGA AGACNACGTG TACGCCCTCA CGCCATGGTC	300
20	GAGGCTCCTG NTGAGCTCCG AGCACACCGC GGTAGCCCCG TTCGTGGTGT GGATGCTCCA	360
	CCCGTTCATG GTGCAGTCGT GGCACCTCGT GGGGGCGTGG TTCCACGGGA GGGCGCCAC	420
	CCCCTTCGCC GCAACCCACG GGAAAGGGGA TCTTCGAGAC NACACNCNAA CAGCCGGGGT	480
25	TCGCGGCCGT TCTTCANCNA NGCNATGGCG AACGACTGTC GGCTGGTGGG AAAGGTGTTG	540
	GTAAANAACA TNCGGATGTG TTGGANGGAN CNCNGGTCCA TNGTGGAAGT TGGTGGCGCA	600
30	CCGGCACCTT TTTNGGCCAT TGTGCGCGA AGGCTTTCCC GCCAACATNA AATNGCACCG	660
	TTCTCCNANT TTGCCCCACT TTTCTGGCCN CNGCCGCCGG GGCCCCNCN NACCNAAACA	720
	ACTTGATGT TTTTNGGGG AANACATNTT CCAACATTTT ACANCCGCNC GACNTTTTTT	780
35	ACNCAATTGG TTCNGGCNC NAATGGAAAT ANTNCTGNAT TT	822

(2) INFORMATION FOR SEQ ID NO: 12:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 743 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

45

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-U72

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

55	GGCACGAAGA GCCCTGTACC GGANAGCATG GAGAACCCTG TTGCGGTGGG CATCATGGAG	60
	GAGCTTGAGG CCCAGAGCGA GGTGTGGAAC CACATTTTGA GATTCATCAC CTCCATGTCC	120
60	GTCAAGTGCG CGGTGGAGCT CAGGGTCCCC GACGCCATCC ACGCCCACGG CGGCAACGCA	180
	ACTCTCCCTC AGCTGGCCGC CGCCGTACAG CTCCCTCCCC CCAAGCTCGC CGACCTCCGA	240
	CGCCTCATGC GCATGCTGGT CCACGCCGGC TGCTTCACCA AGCAGGAANA CNACGTGTNC	300
65	GCCCTCACGC CATGGTCGAN GCTCCTGGTG AGCTCCGANC ACACCTCGGT GGCCCCGTTC	360
	GTGGTGTGGA TGCTCCACCC GTCATGGTC CAGTCTGGC ACTCCTGGG GCGGTGGTTC	420
70	CACGGGAAGG GCGCCACNC CTTTCNCNC NACCCNCGGG AAGGGGATCT TCCANACGAC	480

ACNCGAACAT CCGGGGTTTCG CGGGCGTCTT CAACTANGCG ATGGCGAACG ACTGTCNGCT 540  
GGTGGGAAAN GTNTTGGTAA AAAAACCTTC CGGAAGTGTT NGANGGAACC CCGTCCAATN 600  
5 GTGGAANTTG GTGGCNGCCG GCACCCCTTNC GGGCNATCGT TGTCGAAGNC CTTCCCNAC 660  
NTTANATTNC ACCGTCCTCC AATTNTCCCC ANTTTCTTTN GCCGCNGGNN NCGGGCCCCN 720  
GGTNANCCNA AANCNTTNT TTT 743  
10

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown  
15

(ii) MOLECULE TYPE: cDNA  
20

(vii) IMMEDIATE SOURCE:

- (B) CLONE: U-U68  
25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TGTTCTCTCC TTCGATCACA TCTTTTTGCT CTGGGAAACG TGAGAGGTGA GACGAGGGCG 60  
30 GCAATGACGG CGGGTTTAAG ATGGATTCCT CCTCTGCTTC TTCTTCTTCT GGGCTTCCTG 120  
CTGGTTTTGA ACGGAGGTCG GGGGTGGATT GGAAGCGAGA GGTCTCTGCTG CTCGAGGAAT 180  
35 GCGGAGCAT CGCGGAGGAG CTTGAGAGAG GCCTCCGCGA ACGCGACCAG CGCCGATGCT 240  
TCCTTGAAG AGAGGGCTGT AACCCGGGCA GCAGAAGCCG CAGTCGACGA CCCCAGGAG 300  
GTTGCTTCGA CGGTCCTGAT GACCATAATC AACAGCACGG CTCGCAGATC TCTTGGTTAT 360  
40 CTGTCGTGCG GTTCAGGCAA CCGATCGAC GACTGCTGGC GGTGCGACCC TGATTGGCAT 420  
GTCAACAGAA AAAAGCTCGC TGAAGCTGGC ATTGGCTTTG GACGCAACGC NATANGTGGC 480  
45 CGCGACGGGG AATTTGTTTCG TTGTGACAGA CTCCGGGGAC NATGATCCCC GTGAATCCTC 540  
GCCCCGGAAC ACTTANATAC CCCGTCNTCC AANGAAGTTG CCCCCTCTGG GATCCCCCTT 600  
AAACNCNAAN TGGAAATCTC NCTCNANGGA AGAACTCNTT ATGAACAGCT TTAANACNAT 660  
50 CGATGGACNC NGTGTCTCTG TCCACATTGC CAATGGCGCC TGCNTCACCA NCCAATTTCN 720  
TCCCCAACNT CTTCTTCNT NGCCTCCNCT CCCCAATGCA ACCCNCCGGG AATTCCTNGT 780  
55 CCCCNTCCC CTTCTCCTAT GGATNG 806

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown  
60

(ii) MOLECULE TYPE: cDNA  
65

(vii) IMMEDIATE SOURCE:

- (B) CLONE: U-U69  
70

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

5 GGCACGAGGG AGAACAAAAA TGGCAGCATT CTTGTTCTTC CTCACCATCG CAGCCTTCAC 60  
 TGCCCCATC TACTCTTCTC GTGCACCCTT AACGTCGGCA GCTGTCCGCG ACCCTGAATT 120  
 AGTAGTACAG GAAGTACAAA GAAGCTTGAA CGTGTCCGCG CGGCGACTGG GCTACTTGTC 180  
 10 ATGCGGCACC GGCAATCCGA TCGACGACTG CTGGCGGTGC GACCCTGACT GGGCTGACAA 240  
 CCGGCAGCGG CTCGCGGACT GCGCCATCGG GTTCGGGAAG AACGCGATTG GGGGCAGGGA 300  
 15 CGGCGAGATA TACGTGGTGA CCGACAGTGG CGACNACNAC CCCGTCAATC CGAAGCCGGG 360  
 CACGCTCCGG TACGCCGTCA TCCANGAGGG AGCCGCTGTG GATCATCTTC AAGCGCGACA 420  
 TGGTCATCCA GCTGAAGGAA GGAGCTCATC ATGAAACTCC CACANAGACC ATCGACGGCC 480  
 20 GGGGCGCCAG CGTCCACATC TCCGGGGGGC CGTGCATCAC CACCAGTNCG TCNCCAACAT 540  
 CATCATCCAC GGGCGTCCAC TTCCACNAAT GCAANCAGGG CGGGGAACGC CTTACGTTTCG 600  
 25 CGACTCCCCC AGGGCACTAC GGGTGGCGCA CCGGTGTCCG AACGGCNANG GGGTTTTTCAT 660  
 CTTCCGCGGG AACCACTTCT GGGGTCA 687

## (2) INFORMATION FOR SEQ ID NO: 15:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 741 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 35 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

40 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U84

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

45 TCCACATTGC CAATGGCGCC TGCATACCA TNCAGTACAT CACCAACGTC ATCATCCATG 60  
 GCCTCCACAT CCACGACTGC AAGCCCACCG GGAATGCCAT GGTCCGCAGC TCTCCTTCTC 120  
 50 ACTATGGATG GAGAACCATG GCTGATGGGG ATGCCGTTTC CATTTTCGGC TCCAGCCACA 180  
 TTTGGGTGGA CCACTGCTCT CTGTCCAAT GCGCCGATGG ACTTGTCGAT GCCGTCATGG 240  
 55 GCTCCACTGC CATTACGGTC TCCAACAATT ACTTCACCCA CCACAATGAG GTCATGCTTT 300  
 TGGGACACAC TGATTCTTAT GCAAGGGACA GCATCATGCA AGTAACGATC GCATTTAACC 360  
 ATTTTGGTGA AGGTCTGATT CAGAGAATGC CCAGGTGCAG GCATGGCTAC TTCCACGTGG 420  
 60 TAAACAATGA CTACACGCAC TGGGAGATGT ACGCCATTGG CGGTAGCGCG AATCCAACGA 480  
 TCAACAGTCA AGGCAACCGA TACCTTGCGC CGACCAATCC ATTTGCAAAG GAAGTAACAA 540  
 AAAGGGTGGA CACAGATCAA AGCACGTGGA AAAACTGGAA TTGGANGTCN GAAGGTGACC 600  
 65 TGCTTCTGAA TGGTGCTTTT TTCACCCTTC CCGTGCANGG GCTTTCACCC ANCTACGCAC 660  
 GGGCCTCCAC TTTGGGGGCA ACCCTCTTCC TTNGTTGANA CACTGACTCT GATGCTGGGG 720  
 70 TCCTGTTTTG CCAATTCGGN C 741

## (2) INFORMATION FOR SEQ ID NO: 16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 727 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: U-U89

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGCACGAGTT CTCTCCTTCG ATCACATCTT TTTGCTCTGG GAAACGTGAG AGGTGAGAAG 60  
 AGGGCGGCAA TGACGGCGGG TTTAAGATGG ATTCTCTCTC TGCTTCTTCT TCTTCTGGGC 120  
 TTCCTGCTGG TTTTGAACGG AAGTCGGGGG TGGATTGGAA GCGAGCGGTC CTCTGGCTCG 180  
 AGGAATGGCG GAGCATCGCG GAGGAGCTTG AGAGAGGCCT CCGGAACGC GACCAGCGCC 240  
 GATGCTTCCT TGGAAGAGAG GGCTGTAACC AGGGCAGCAG AAGCCGCANT CGACGACCCC 300  
 GAGGAGGTTG CTTGACGGT CCTGACGACC ATAATCAACA GCACGGCTCG CAGATCTCTT 360  
 GGTATCTGT CGTGCGGTTT AGGCAACCCG ATCGACGACT GCTGGCGGTG CGACCCCGAT 420  
 TGGCATGTCA ACAGAAAAAA GCTCGCTGAC TGCGGCATTG GCTTTGGCCC GCAACGCGAT 480  
 ANGTGGCCGC CACNGGGANT TGTNCNTTGT TGACAGACTC CGGGGACGAT GATCCCGTGA 540  
 ATCTCCCCC GGAACACTTA ATATTCCCCG TCATCCAGA NCTNCCCCTC TGGATCNCCT 600  
 TTTAAACACG ACATTGGAAA TCNCCCCCNG GAAGAACTCC TTTNTAACCG CTTTNNACA 660  
 TCNATGGACN CGTGTCCACN TTCCACNTTT GCCAATGGCG CCTGCCTCNC CANCCNATTT 720  
 AATCNCC 727

## (2) INFORMATION FOR SEQ ID NO: 17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: U-U115

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GGCACGAGGG AGAACAAAAA TGGCAGCATT CATGTTCTTC CTCACCATCG CAGCCTTCAC 60  
 TGCCCCCGTC TACTCTTCTC GTGCACCCTT AACGTCAGCA GCTGTCCGCG ACCCTGAATT 120  
 AGTAGTACAG GAAGTACAAA GAAGCTTGAA CGTGTCCGCG CGGCGACTGG GCTACTTGTC 180  
 ATGCGGCACC GGCAATCCGA TCGACGACTG CTGGCGGTGC GACCCTGACT GGGCTGACAA 240  
 CCGGCAGCGG CTCGCTGACT GCGCCATCGG GTTCGGGAAG AACGCGATTT GGGGCAGGGA 300

CGGCGAGATA TACGTGGTGA CCGACAGTGG CGACNACGAC CCCGTCAATC CGAAAACGGG 360  
CACGCTCCGG TACGCCGTCA TCCAGGAGGA GCCGCTGTGG ATCATCTTCA AGCGCGACAT 420  
5 GGTATCCAG CTGAAGGAGG AGCTCATCAT GAACTCCAC AAGACCATCG ACGGCCGGGG 480  
CGCCAGCGTC CACATCTCCG GCGGGCCGTG CATCACCACC AGTACGTCAC CAACATCATC 540  
10 ATCCACGGCG TCCACATCCA CGAATGCAAG CAGGGCGGGA ACGCGTNCGT TCGCNACTCC 600  
CCAAGGGCAC TACGGGTTGG CGCACNGTGT TCNGACGGCG ACGGGTGTCC ATCTTCCGCG 660  
GGAACCACTC TGGGTCCAAC CACTGCANCG CTTGTTCCTAA CTTGGCCAC CNAANTGGGC 720  
15 CTTCCNTCCC AACCCCCATT TCCTTGGGAT TNCCCCCGC CAATTCCCC ATTTTCCAAC 780  
NAACTTNCTT TGAACCCNCC CNTGAANAAG GTCCTTGCTG CTGGGTCCCA CCAACAATTT 840  
20 NA 842

## (2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 724 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
35 (B) CLONE: U-U117

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

40 GGCACGAGTC TCCTTCGATC ACATCTTTTT GCTCTGGGAA ACGTGAGAGG TGAGACGAGG 60  
GCGGCAATGA CGGCGGGTTT AAGATGGATT CCTCTCTGC TTCTTCTTCT TATGGGCTTC 120  
CTGCTGGTTT TGAACGGAGG TCGGGGGTGG ATTGGAAGCG AGAGGTCCTC TGGCTCGAGG 180  
45 AATGGCGGAG CATCGCGGAG GAGCTTGAGA NAGGCCTCCG CGAACGCGAC CAGCGCCGAT 240  
GCTTCCTTGG AAGACAGGGC TGTAACCAGG GCAGCAGAAG CCGCAGTCGA TGACCCCGAG 300  
50 GAGGTTGCTT CGACGGTCCT GACGACCATA ATCAACAGCA CGGCTCGAAN ATCTCTTGCT 360  
TATCTGTCGT GCGGTTGAGG CAACCCGATC GACNACTGCT GCGGGTGCGA CCCCATTGG 420  
CATNTCAACA GAAAAAGCT CGCTGACTGT GGCATTGGCT TTGGCCGCAA CCGATANGT 480  
55 GGCCGCGACG GGGANTTGTN CGTTGTGACA GACTCCGGGG ACGATGATCC CCNTGAATCC 540  
TCCCCCGGGA AACTTANAT NCCGTCNTC CNNGAANTTT CCCCTCTGGA TCNCTTTAA 600  
60 ACCCACNTGG ANATCCCCN CNAGGAAGAA CTCCTTATGA ACNGCTTTTT AAAACATCGA 660  
TNGGACCCNG TTTCCACTC CNCATNGCC NAATTGGGCG CCCTGGCCNT CCNCCNTCC 720  
CCAA 724

## (2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:  
70 (A) LENGTH: 797 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

- 30 -

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

5

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-U80

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGCACGAGGG ACAAGCGATG GCAGCAGAAT TGTCTCCAC GCTGAGCAAG AGCATCTTTG	60
15 AAGGAGCCGG TGGATCTTAC TCTACTTGGT CAGGTGCCGA TCTCCCCCTT CTTACTGATG	120
CAAAGCTCGG CGGAGGCAAG CTTGTCCTGA AACCCTGGG CTTGGCGTTG CCTCACTATT	180
20 CCGACTCATC GAAAGTCGGC TATGTTCTTG AAGGAAGAGC GGTGGTGGGG CTAACACTCT	240
ATGGAGAGAC CGAGCAGAGG ATACTGCTGC TTGAGAAGGG AGATGTGGTA GCGGTGGTCA	300
TGGGGAGCCT CACGTGGTGG TACAACGAGG AGGAGGACTC CGACTTCTCC ATCGCCTTCT	360
25 TAGGCGATAC CGCGACAGCT GTGCGACCGG GCGACATCGC CTAATTCTTC TTGGCAGGAT	420
CCCTAGGAAG TGCTCCATGG CTTTTGACG GAAATTCCTC ANCAGGGCCT GCGGTTTAAG	480
GGGATGCGGA AGCTGANGAG CTCTTCGGAA GCCAACCTGG TACTCTAATC ATCACACNGC	540
30 AGCAAAAGCT GCCTGGCCTC AGANCATCCC GAGCTGACAG CNAAGGGATA TCNTAAACGC	600
TGANCGCGTA NCGGCATATA TCAATGTGAA AAGTGGTGGC TGTTCTGCCT CCGTGACCCT	660
35 TNATNAACTG GCNGCNCCTG GAAGATCAGG TTCTCCGTCN ACCTCCAAAA ATCCANCCTA	720
ACCCCGTGCC TTGCCGGGGT TCTTCNTTGA ATCNCCTGTT CANCTGAAAT TTTTCCCCAA	780
GGCCNTGGAA CAATTCT	797

40

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 742 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

45

(ii) MOLECULE TYPE: cDNA

50

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-U90

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GGCACGAGAT GACTCTCTCG GCGGTAGCAT CGGATGCCGA TGATTGGGTC GCTTATACAT	60
60 TCGCTTCGCG ATACGTTTCG GAGGCTCTTC CCCGTTTCAG GATACCGGAG CAGTCGATCC	120
CCAAGGATGC GCGGTACCAG ATCATCAACG ACAGAGCTGAT GCTCGACGGG AACCCGCGGT	180
65 TGAATCTGGC GTCGTTCTGT ACGACGTGGA TGGAGCCGGA GTGCGATCGC CTCATCATGG	240
CGGCCGTCAA CAAGAACTAC GTCGACATGG ACAGGTACCC CGTCACCACC GAGCTCCAGA	300
ATCGCTGCGT AAATATGATA GCCCACCTTT TCAATGCCCC AATTGGGGAA NACGAAACGG	360
70 CTGTTGGAGT TGGAACTGTG GGTTCCTCCA GAAGCAATCA TGCTTGCAAG ACTTGCAATC	420



- 31 -

AAGAGGAAAT GGCAGAACAA AAGAAAGGCA GAGGANAAGC CTTACGACAA ACCCAACNTT 480  
 GTTACCGGTG CAAATGTTCA GGTGTGCTGG GANAAATTTG CAAGGTATTT TGAAGTTTGA 540  
 5 ACTGAAAGAA ATTGAAGTTG AAAGAAGGAT ATTATGTTAA TGGATCCTGC CAAGGCAGTA 600  
 NAAATGGTTG ATGAAAAATA CATATGTTTT TGCTGCCATC TTTGGGTTCA ACTCTCCCTG 660  
 10 GGAAATTTG AANATGTTAA CCTTCTAAAT GATCTCCTGA CNGAAAAAAA CCCAGAAACT 720  
 GGGTTGGACC CCCNTACTT GT 742

## (2) INFORMATION FOR SEQ ID NO: 21:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 807 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 20 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U92

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GGCACGAGCT CTAGCCGATG ACTCTCTCGG CGGTAGCATC TGATGCCGAT GATTCGGTCTG 60  
 CTTATACATT CGCTTCGCGA TACGTTTCGG AGGCTCTTCC CCGGTTTCAGG ATACCGGAGC 120  
 35 AGTCGATCCC CAAGGATGCG GCGTACCANA TCATCAACGA CGAGCTGATG CTCGACGGGA 180  
 ACCCGCGGTT GAATCTGGCG TCGTTCGTGA CGACGTGGAT GGAGCCGGAG TGCGATCGCC 240  
 40 TCATCATGGC GGCCGTCAAC AAGAACTACG TCGACATGGA CGAGTACCCC GTCACCACCG 300  
 AGCTCCAGAA TCGCTGCGTA AATATGATAG CCCACCTTTT CAATGCCCCG ATTGGGGAAN 360  
 ACNAAACGGC TGTGAGGTT GGAAGTGTGG GGTCTTCAAA AGCAATCATG CTGTCAGGGC 420  
 45 TTGCATTCAA GAGGAAATGG CANAACAAAA GAAAGGCAGA GGANAAGCCT TACGACAAAC 480  
 CCAACATTGT TACCGGTGCA AATGTTTCNGG TTTTGCTGGG AANAAATTTG CAAGGTATTT 540  
 50 TGAAATTTGA ACTGANAGAA NTGAANTTGA AAGAAGGATA TTATGTTTAT GGATCCCNCG 600  
 CCAAGGCAGT ANAAATGGTT GATGAAAATA CCAATTTNTG TTGCTTGCCC ATCTTTGGGT 660  
 55 TCCACTCTCN CTGGGANAAT TTTGAAAAAT GTTNAAGCTT TAAATGATCT CCNGGACCNA 720  
 AAAAANNCCC NNAANCTNGG TTGGGACCCC CCCNTACCTT TTCNATNCCT GCCANTTNGG 780  
 GGATTNNNTA NCGCCTTTCC TNCTATC 807

## (2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 770 base pairs  
 (B) TYPE: nucleic acid  
 65 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

70 (vii) IMMEDIATE SOURCE:

(B) CLONE: U-U91

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GGCACGAGAG AAAAAATTGT AAAGTTTGAC TTTCATGGAC AGCCTGCGGA GCTCAAGCAT 60  
 GGTAGCCTTG TCATAGCAGC AATTACAAGC TGCACAAACA CATCAAATCC CAATGTTATG 120  
 10 CTTGGTGCTG GTCTTGTTGC AAAGAAGGCC TGTGAATTAG GTCTACAGGT TAAGCCTTGG 180  
 ATCAAAACCA GCCTTGCTCC AGGTTCTGGA GTTGTTACCA AGTATTTGCT TAAGAGTGGC 240  
 15 CTACAAGAAT ATTTGAATCA GCAAGGATTT AATATTGTTG GGTATGGCTG CACAACATGT 300  
 ATCGGAAACT CTGGGGATCT TGATGAGTCT GTGGCTGCTG CAATTTCCGA TAATGATATA 360  
 GTTGCTGCTG CTGTTCTATC TGGAAATAGG AATTTTGAGG GACGTGTGCA TCCATTGACA 420  
 20 CGAGCTAACT ATCTTGCTTC ACCTCCGCTT GTTGTAGCTT ATGCGCTTGC TGGAACAGTT 480  
 GACATTGATT TTGAAAAAGA ACCCAATTGG AACAGGGGAA GGATGGGAAA AAACATATAC 540  
 25 TTCCAGGATA TATGGCCGTC CACTGAANAA ATTGCACAGG TTGTGCAATC CANTGTTTTT 600  
 GCCTGAAATG TTCAAGAATA CCTATGAAGC AATCACCAA GCACCCTATG TTGGAACCAA 660  
 CTGACTGTTC CCNGCCACAC TCTTTATTCA TGGGACCCAA TCCNCNTACA TCTTAACCAC 720  
 30 CNTATTTTAA GGANATGACC ATGGCCCNCC TGTCCNCATG GGGTGAAAAA 770

## (2) INFORMATION FOR SEQ ID NO: 23:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 810 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

40 (ii) MOLECULE TYPE: cDNA

45 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U96

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GGCACGAGAG GGCCGTTTCCT TTTGTGCTC GCTTTGCTGC CTCCTCGTTC GTCTTTTCCG 60  
 CGAATTTTAC CGGCCATGAA CAGCCTTCGG AGCCTTCCGA CATCCTCCGC TCCGCCCTCG 120  
 55 CCGGTCCCGA GAGGACGTTT GAGTAGGCCA CCGACCTTGA ATCTGGGGGT GATACGACCA 180  
 CATCATCTTC GTGTAAATGT CGCCAGGAGT GCATGTTCCA AGTCTTCTGC AAGTCCTGAG 240  
 AAGACTGGTG CTGAAGTGCA AGATCAGAAG TCTGAGATAT ATAGCAGTGA TATGACAAAA 300  
 60 GCAATGGGTG CAGTGCTGAC ATATAGGCAT GAGCTTGGA TGAATTATAA TTTCATCTAC 360  
 CCAGGATTGA TTGTTGGTTC TTGTCTACAG ACCCCATCAG ATGTTGATAA GCTTCCNAAA 420  
 65 GATTGGGGTT GAAGACCATC TTTTGCTTGC AGAAGGACTC GGATCTTTGA ATATTTTGGG 480  
 GTTGAAATTG GTGCAATTCC NTGAATATGC CATGCAATGT GGTGACATTG AACATCTTCN 540  
 TGCTGAAATC AGGGATTTTG ATGCATTTGA TTTGAAGATG ANACTTCCTG CNGTANTTAC 600  
 70 NAATTATACA AGGCTAATTA ATCCGAATGG TGAATGACT TATTTTCNCT GTACANCCNG 660

GCTTGGA AAA CGCCTGCANT TGCNTTGGCA TACNTGTTTT TGGGTTNAAG GCTATGAACT 720  
 5 GAATGAAAGG GCCCCNCTAC TGCNAAATTA NCCAACTTGC TCCCCNAAAT TTGGTGCTAT 780  
 AAAAAANTGCC ACCNTTGATA TGCTTATNGG 810

## (2) INFORMATION FOR SEQ ID NO: 24:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 765 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

20 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U103

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

25 GGCACGAGCT TGGCTGTAGT CTTCTTCTCA AGTAATCTTC GTCTTCCTGA TTTGCTTGGT 60  
 TGGTGGTCGG TTGCAGGGCG AAGGGATGGG GATGGGGAGG CCGAGCGGAG CTTGGTCGAC 120  
 30 CCCGTGGTTG TGGGTGGTTC TTGTGCATTG GCTCCTCTGG GCCACCGAGA GGAGGCGAGG 180  
 GGGCGTGGTG GAGGCCTCCC ATGTGGAGTT TGCATCCCTC CAATCTGTTC CTGCCTCCGT 240  
 35 CGTCGACAAC AGGCTGAGGA CTGGGTATCA CTTCCAGCCC CCGAGGAACT GGATCAACGA 300  
 TCCAAATGGA CCCATGTACT TCAATGGCGT CTACCACCTC TTCTACCAGT ACAACCCCAA 360  
 TGGCTCCGTG TGGGGTAACA TCGTGTGGGC CCACTCGGTG TCGACCGACC TCGTCAACTG 420  
 40 GATAGCACTC GACCCGGCCA TCCGCCCCAG CAAGCCATTC CACATCAACG GATGCTGGTC 480  
 CGGCTCCGCC ACCGTCTCC CCGGCAACAG GCCTGCGATC TTCTACACCG GCATCNACCC 540  
 45 CCANCANAAA CAACTGCANA ACNTTNCNTN CCCAAGGATC TGTCCAACCT TACTCCCCNA 600  
 NTGGGTCAAC CCCACTNCAA CCCCCTGATC CCCCTGGCGA CGCATCAACN CCACCCCTTC 660  
 CNCNAACCCN AATACGGNTT GGCGCNGTCC CNGCACCCNC TGGAACCCCT TNGTNGGGAA 720  
 50 CNANTTGAAN CNGAAGGGGA AAGGCNTTCT TTNCCGAACA GGGAT 765

## (2) INFORMATION FOR SEQ ID NO: 25:

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 774 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

60 (ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 65 (B) CLONE: U-U93

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

70 GGCACGAGCG GAGAANGCAA TCTCGCTCTC TCTCTACTGC ATCGCGGCTC TCGTCCTCGA 60

- 34 -

TTACTTGAGA TATGGCAGGA AAGGGCGAGG GGCCGGCGAT CGGGATCGAT CTCGGCACCA 120  
 CGTACTCGTG CGTCGGGGTG TGGCAGCAGC ACCGGGTGGA GATCATCGCC AACGATCAGG 180  
 5 GGAATCGTAC CACCCCCTCC TATGTGCGCT TCACCGACTC CGAGCGCCTT ATCGGCGACG 240  
 CTGCCAAGAA CCAGGTCGCC ATGAACCCCA TCAACACCGT CTTTGATGCA AAGCGTTTAA 300  
 10 TTGGTAGGCG ATTCACTGAT TCATCTGTCC AGAGTGACAT CAAGCTCTGG CCTTTCAAGG 360  
 TCATTCTTGG TCCAGGTGAC AAGCCCATGA TTGTGTCCA ATACAAAGG GAGGATAAAC 420  
 AGTTTGCAGC TGAAGATATT TCTTCCATGG TTTTGATAAA GATGAAAGAA ATTGCTGAAC 480  
 15 CTACCTGGGG TCTGTTGTCA AGAATGCCGT CCTCACTGTT CCCGCTTACT TCAATGACTC 540  
 NCAACGCCCA GCCACAAAGG ATGCTGGTGT CATTGCTGGT CTCNATGTTA ATGANAATCA 600  
 TCAATGANCC CCCAGCACTG CTATTGCTTT ATGGCCTTGA CAAAANGCTA CTATTGTTGG 660  
 20 TGAAAAAAT TTCCTCATCT TCCATCTCCG GTGGGTGGCC TTTTGANTTC NCCTTCCTNA 720  
 CCATCCAAGA AGGTTTCTTT NAAGTCAAGG CCCTGCTGGT GANACCCANC TTGG 774

25 (2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 786 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

35

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U125

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GGCAGGAGCT AGTCTCGAGT TTTTTTTTTT TTTTTTTTAA AATTGAAATT AGATGCGATT 60  
 45 TCGAATAGCA AACATAGTTC AGGATAAACC AACACATTG TACCGAATTC GATAAGCTTA 120  
 GGAAACTAAA TTGCGTAAAC GAAACACTTG CATGAAAGCC TATATAATAT AAGGCCGACT 180  
 50 AGGGACNAAA TAACTTAATC GACCTCCTCG ATCTTTGGAC CAGCGCCGCT GCCACCAGCA 240  
 GGAGGAGCAT CATCATCCAT ACCACCAGCC ATGTCAGCAC CTGCTCCCTG GTACATCTTG 300  
 GCGATGATGG GATTGCATAT GCTCTCCAGC TCCTTCATCT TGTCATCGAA CTCGTCGGCT 360  
 55 TCTGCCAACT GGTGCGCATC GAGCCATTGG ATGGCCTGCT CGATCGCATC CTCCGATCTT 420  
 CTTCTTGTCG GCAGCAGCAA GCTTGGAGGC AATCTTGTCG TCGTTAATGG TGTTCTCAT 480  
 GTTGTNAGCA TANTTTTCCA GANCAATCTT CCGATTCCAC CTTCTTTTTT ATGCTCCTCC 540  
 60 ATCTTCCTGA CTTGTTACTT CTCGCTTCC CTGCACCATT TTCTCAATCT CCTCCTTGCT 600  
 GACCTACCTT GTCCTTGGTG AAGGTGATCT TGTTCTCTGT CCAGTGGTCT NTCNTCNGCA 660  
 65 GAAANATTCC AGAATACCAT TGGGGTTCCA AATGTTNCAA AACCAAACCC GGTGGATTCT 720  
 TGAAGGAAAC CCCCCCTAA GGGCCCCAGG GTGGGAAATC CCCCCAAAAA ACCCCCAAAT 780  
 TTTCCC 796

70

(2) INFORMATION FOR SEQ ID NO: 27:

- 35 -

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 486 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

GGCAGGAGCG AGTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTACAAG GNAACCATAG      60
ACATTACACC AACATAGAT GTCAACAATA CATGCCAAGC ATACCATTGC TTATTCCTTC      120
AGACCTCCGA TAGGACTTCC ACGCACACCA ACAGAGAGAA CTAAGACAGC AAAGCAGCGG      180
ACACATACAG CCCAAAAGGG TNNGTGACCC CCGCGGAGGN GGAGCNCCAG GTGAAGGGTG      240
GATTCCCTCT GAATGTTGTA TTCTGNCAGG GTGCGCCCGT CCTCNNTTTG NTTCCNTCT      300
NANATCNCCC NCTGNTGATC TGGTGGNAAT CCCCCCTTG TCCTGTGATT CTTGCTCTTG      360
ACNTTTTTCT CCCNTGTCNN ANCTCTCTNC CTNCTCTGGG TTTGGGTCT TCCCCTGTTG      420
NANCNNTCTN TTNNCNTATC ATCTTGTNCT CCNNCCNCCN CNCCTNTCNT TTCCTCNNNN      480
GGTNNA

```

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 791 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```

GGCAGGAGTG ACAATGTCAA GGCCAAGATT CAGGATAAGG AGGGCATTCC CCCCAGCCAG      60
CAGAGGCTCA TCTTTGCCGG CAAGCAGCTC GAGGATGGCC GCACCTTGGC TGATTACAAC      120
ATCCAGAAGG AGTCCACCCT CCACCTTGTC CTCCGCTCC GTGGTGGCAT GCAAATCTTC      180
GTCAAGACTT TGACTGGGAA GACCATCACC CTTGAGGTGG ANAGCTCGGA CACCATCGAC      240
AATGTAAAGG CCAAGATTCA GGACAAGGAG GGTNTTCCCC CGGACCAGCA AAGGCTCATC      300
TTTGCCGGCA AGCAGCTTGA GGATGGCCGC ACCCTGGCAG ATTACAACAT TCAGAAGGAG      360
TGTACCCTTC ACCTTGCTGCT GANACTTAGG GGTGGCATGC ANATCTTTGT TAAGACNCTC      420
NCAGGGGAAG ACCATTACCT TGGAGGTGGA NANCTCNGAC ACGATTGATA ATGTCNAGGC      480
AAAGATCCAN GACAAGGANG GGATTCCACC GGATCAGCAN ANGCTGATCT TTGCTGGGAA      540

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- 36 -

ACACTGGANG AAGGGCGCAC CCTGGCAGAT TNCNACATTC CNAAAGAATC CACCTTCACC 600  
TGGTGCTCCC CCTCCGCCGG GGTCCCTAAC CCTTTTGGGC TGTATGTNTC CCCTGCCTTT 660  
5 GCTGTCTTAA TTCNCTCTGT TGGTGTTCGT TGGAAATTCC CTAATCCNGA AGGTTCTTNA 720  
AAAGGAAATN AANCCNNTTG GGTTCCTCCC TTTGGCCTTT TTTTGTGTTG AAAATCCTNT 780  
10 GTTTTGGTG T 791

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:  
15 (A) LENGTH: 814 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA 20

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-U120 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GGCACNANCC CGCTTCGGTA GCCATTATTG GTGCCGCTAG AGCGAGTGCT GAGATGGCTT 60  
TGAGGGCCTT CTCCCCCTC TGCATCGCTC TCGTGGTGAC GCTCTCACCT CTGTGTGATG 120  
CCACTTCGCC TTACTIONACC ATCACACCGC CCACCCCGT GGCCAAGCCG CCTTCAGTTG 180  
35 AACCAACCACC CTACCACGGC CCTCCGACNA CCCACCCTAA GCCACCGAGT CATGGTGGCC 240  
AACCTCCGTC CCACCATCAC CCAACACCAA TCTACGGTGC ACCCCCTCCG CAACACCACC 300  
ACCACCACCA ACACCACCAC CAACCTGCAC CACCAACTCA CGCANAAACAC CCTCCGTAAT 360  
40 ACCACATGCC TTCCCCGCCG CCGCATGGCC AGCACCCGTC ACCACCGTCA CATGATTATC 420  
CCGTACCTCC TGCTCACAAG CCCCCTAACTC CGCCGCCGGT TTACAAGTCT CCACCACCGA 480  
45 NCCACCGTCC TTACCCTCCA TCGACGCCAC CCCACCATCC GAAGCACCCG CCTTCTCAGC 540  
CGAAGCCGTC NTACAAGGCC CGCCACCATN CAAGAATATC CCTGANCACT CTCCACCGCC 600  
GCGTCACTAT CATTCTCCGT CTTACCACACC ACCACCACCA CCATACAAAA TAATCTCGTT 660  
50 TTGCCATCTT CTCCCGTTTG AAAAAAANN CAANTGTCCT TTTTATTTAA CCNAATCCAN 720  
GGGGTTTTTN TTAANATTTN AANAAANCNA ANTNTTTTCC CCCCCNTNTT GGTTNATGGC 780  
55 CTATGGGTTT GTTCTCTTC TTGGCTTTTC CCGG 814

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:  
60 (A) LENGTH: 742 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA 65

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-U126 70

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

5 GGCACGAGGT TGTGCCTAAC AGAGAGAGAG AGAGACAGAC CGATAGCCTC CTCATTCACT 60  
 ATGGCGATCC GATCGCCAGC TTCGCTGCTG TTATTTGCGT TTCTGATGCT TCGGCTCACA 120  
 GGAAGACTGC AGGCCGGGCG CAGCTCATGC ATTGGCGTCT ACTGGGGACA AAACACAGAC 180  
 10 GAGGGAAGCT TAGCAGATGC TTGTGCCACA GGCAACTACG AATACGTGAA CATCGCCACC 240  
 CTTTCAAGT TTGGCATGGG CCAAATCCA NANATCAACC TCGCCGGCCA CTGTGACCCT 300  
 CGGAACAACG GCTGCGCGCG CTTAAGCAGC GAAATCCAGT CCTGCCAGGA GCGTGGAGTC 360  
 15 AAGGTGATGC TCTCCATCGG AGGTGGCGGG TCTTATGGCC TGAGTTCCAC CGAANACGCC 420  
 AAGGACGTGG CGTCATACCT CTGGCACAGT TTCTTGGGTG GTTCTGCTGC TCGCTACTCT 480  
 20 CNACCCCTCG GGGATGCGGT TCTGGATGGC ATANACTTCA ACATCCCCGG AGGGAGCACA 540  
 GAACACTATG ATGAACTTGC CGCTTCTCTC CNAGGGCTAC AACGAACAGG AAGCCGGAAC 600  
 CAAAAAAGTT TCACTTGAAT TGCTGCTCCC NCANTGTCCT TTCCCCGATT ACTGGCTTTG 660  
 25 GCAACCCACT CAAAACAAA TNTCTTCNA CTTCNTGTT GGGTTGCNAA NTTCCNTTCC 720  
 CAANCAACC CCTTCNTTT GC 742

## 30 (2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 794 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

40

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U129

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GGCACGAGGG CGTGGCGGAG ATGGGGAGCT GCGGGGCTCT GTTGCGAGCGG CGGCTGCTGT 60  
 50 TGCTCTCTGC TTTGGCGGTG GCTGTTCGTG TGAAGGCACT CAGCANANAC NATTTCCCCG 120  
 CCGGCTTCAT TTTTGGCGCA GGCACCTCCG CTTATCAGGT ANAAGGTGCA GCTGCAGAGG 180  
 GGGGAANAAC ACCCAGCATT TGGGACACGT TTACGCATGC AGGGAGAACT TTCGACCAGA 240  
 55 GCACCGGAGA CGTAGCAGCT GATCAGTATC ACAAGTACAA GGAAGATGTG AANCTGATGC 300  
 ATGANATGGG CTTGATGCT TACAGATTCT CCATCTCTCG GTCCANAGTT ATCCCCAATG 360  
 60 GTCGAGGGCC TGTGAATCCA CAAGGCTTGC GGTACTACAA CAACCTGATC GATGAGCTCN 420  
 AAAGATATGG AATCCGAGCC TCATGTCACT CTTTACCACT TCGACCTTCC GCAAGCACTG 480  
 GAANACGAAT NCGCCGGGCA GCTGAACCCA AAGATCGTAN ANGACTTCAC CGCTTACGCC 540  
 65 AACGTTTTGC TTCANCNAAT TTGGGGATCN AATCTAGCAC TGGATCNCCC ATCAATGAAC 600  
 CAACATANAT CCCGTCCTCC GCCACNAATT CCGCATCTTC NCCCCTGGCC CTGCTCTTT 660  
 70 ATCCCTTNCG CCTCCAACG CNCCAAGGGC NACTCCCCC CATTTTNAAN CCCATNNNNT 720

CCNCCCCCCC CAATTAACCC NTTCTTGCTC TTCCCCCTTG CCTTCANCCA ACCCGCCCNT 780  
 TTTCNAAAA AANA 794

5 (2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 799 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U130

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GGCAGGAGCC GGCCTCAGGC ATATGGTGCG GTCGCTACAC GTGTTCAAGC AAGGCCGGGA 60  
 25 GCCGGCCAGG ATCATCAGGG AAGCACTGTC GAAGGCGCTG GTGAAGTACT ACCCCTTCGC 120  
 GGGGCGGTTC GTGGACNATC CCGAGGGCGG CGGCGAGGTT CGTGTGCTT GCACTGGCGA 180  
 GGGCGCTTGG TTCGTCNAGG CCAAGGCGGA CTGCAGCTTG GAGGACGTGA AGTACCTCGA 240  
 30 TCTCCCGCTC ATGATCCCTG AGGACGCGCT CCTGCCCAAG CCCTGCCCGG GACTGAACCC 300  
 CCTCGACCTC CCTCTCATGC TGCAGGTGAC ANANTTCGTG GGCGGCGGAT TCGTGGTCGG 360  
 35 CCTCATCTCC GTCCATACCA TCGCCGACGG CCTCGGCGTC NTCCANTTCA TCAACGCCGT 420  
 CGCCCGAAAT CGCCCGTGGC CTGCCNAANC CCACCGTGGA NCCTGCATGG TCCCGGGANG 480  
 TCNTACCCAA CCCACCTAAG CTGCCTCCCG GTGGCCCGCC CGTGTTTCCC CTCCTTCAAN 540  
 40 CTGCTCCACG CCACCGTCGA ACTATCCCTT GACCACATCC ATCACGTCAA GTCCCCACAC 600  
 TTTGGANCTC ACCCGGCCAA CGCTGCTCTA CCTTCCACNT CCCCATCCCC AACCTGTTTG 660  
 45 NAATCCCGCA CGCCCGCCN TCNACCTTGG AACCCAAGGC NTTTCCAANC TTGCAACCC 720  
 TTTTTTCCTT TCCTTCCCCC CCAAAANAA CTCCCCCA CCCTTGTTTT TGCNCCAAG 780  
 50 TTTTTTCCTT CCTTGCCCC 799

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 759 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U43

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GGAGGTTGTT GTTCATGTCC CTAATTGCGG GTCTCCTGTA CAGATTGAAT TTCAAGTAAC 60  
 70 TAATAGCAGT GGCTACTTGG TGCTTCATTG GGTGCAATT CATAATAGAA GGAATAACTG 120



5 GTCAC TTCCT TCTCGTCATC CTGATGGAAC AAAAGTATAC AAAAACCAGAG CTCTCAGGAC 180  
 ACCTTTTAAA AAATCTGGTT CCACATCATC AGTAAAAATG GAGATTGATG ATCCTGAAAT 240  
 ACAAGCAGTT GAGTTTCTCA TATTTGACGA GTCAGAAAAC AAATGGTTTA AACATAATGG 300  
 TCAGAATTC CATGTCCAGT TATTAACA GGGCTATCAA AATCAAAATG TTTTGGCCTC 360  
 10 TGTAATCCA AATGTTTCAC TGCCANAAAG AACTTGTGCA GATTCAAGCT TATCTTAGGT 420  
 GGGANANAAA GGGTAGGCAA ACATATACAC CTGATCAAGA AAAGGATGAG TNTGAAGCAG 480  
 CTANAAGTGA GTTTGCTANA AAAACTAAGT NNAAGTACTT CTGTANANGA NCTCCGATCT 540  
 15 AAATTGACAA AAAACNCCAC TGCTGGAGCG GACAAATCCG TCAAAGTTGA AACTATCAAA 600  
 AGTGGGATCC GGATGATCTT NTGCAAGTTA CANGCATACT TCCNATNGGA AAAACCGGGA 660  
 20 AACCATNTTA TCCCCNGAA AAACACTNAT GGAATTGAAG AAACCAGGGA AANACTGCCC 720  
 ATGAATTAATA TAAANGAACN CNCCTNCAAA CTNAGGGAA 759

## (2) INFORMATION FOR SEQ ID NO: 34:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 785 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

35 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U70

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

40 GGCACGAGAG AGAGAGAGAG AGAGAGAGAG AGAGAGAGAG AGAGAGAGAG AGAGAGAGAG 60  
 AGAGTAATCG ATTTAGCGTG CAAAGTACTG CAGCAGAAGC CATGGCATCC ANGGCCTCAG 120  
 45 CNTCGGCTGC CCTCTTCCTT GCTCTCAACC TTGTCTTCTT TGCACTCACC AGTGCTTGTG 180  
 GCACCACTTG CACCCCCGCC ACTAAGCCCC CACCGAGCTC TTCCCATGGC AAATGCCCCG 240  
 50 TCGACACCCT CAAGCTGGCC TCCTGCGCCA ACGTGCTCAA TGGCCTGATC NNGGTCGGCG 300  
 TCGGCAAGCT CCCGAAACAG CCGTGCGAGT GCTGCNCTCT GCTCGATGGC CTCGTCGACC 360  
 TCGAGGCCGC CGTGTGCCTT TGCNCTGCTA TCANGGCCNA TGTCCTTGGC ATTCATCTCA 420  
 55 ACCTCCCCAT CNNCTTCAGC CNTCTCCTCA ACTACTGCGG TNAGAAGGCT CCCACCGGTT 480  
 TCCAGTGCCC TTGAGCTCCC CCTGCGGATC ACATNTCGA TCCTCTTTGC CCGTGGTGAA 540  
 60 TTTTNTTGAG CATTCCTTTG TGTCTTTACT TCCCTTTGTT TTTGGCTTTT TGATGACGAA 600  
 AGTGTTGAGT GTTGATATGA AGGGCCANTG GCGCTTTCNT GTTAATGTGA CCTGTCNTTC 660  
 CCTTTTATT TCCACNNCTT GTTGANTTTC CCTCTCGGGT TTGTTAATGA AGATCNATGC 720  
 65 ATTCAATTNT TAATATTTCT GCTGCCTTCC AANAAAAAAT ANNANTNCT CCNNGAANTC 780  
 TTCCT 785

## (2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 784 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

	CGGCACGAGG AAANGACNAG CGATGGCAGC AGAATTGTCT CCCACGCTGA GCAAGAGCAT	60
	CTTTGAAGGA GCCGGTGGAT CTTACTCTAC TTGGTCAGGT GCCGATCTCC CCCTTCTTAC	120
	TGATGCAAAG CTCGGCGGAG GCAAGCTTGT CCTGAAACCA CTGGGCTTGG CGTTGCCTCA	180
	CTATTCCGAC TCATCGAAAG TCGGCTATGT TCTTGAAGGA AGAGCGGTGG TGGGGCTAAC	240
	ACTCTATGGA GAGACCGAGC AGAGGATACT GCTGCTTGAG AAGGGAGATG TGGTAGCGGT	300
	GGTCATGGGG AGCCTCACGT GGTGGTACAA CGAGGAGGAG GACTCCGACT TCTCCATCGC	360
	CTTCTTAGGC GATACCGCGA CAGCTGTGCG ACCGGGCGAC ATCGCCTACT TCTTCTTGGC	420
	AGGATCCCTA GGAGTGCTCC ATGGCTTTTC GACGGAATTC CTCANCAGGG CCTGCGGTAT	480
	AAGGGATGCG GAANCTGAAG AGCTCTTCGG AAGCCAACCT GGTACTCTAA TCATCNCCT	540
	GCANCAAAAG CTGCCTGGCC TCANAAGCAT CCCGAGCTTG ACNGCGAAGG GATAGTCNTN	600
	AACNCTNANC GCGTTNCGGC ATATATCAAT GTNAANAGTG GTGGCTGTGC TGCGTCCGTG	660
	ACACTTNATG AACTGGCCGC GCTGGGAAGA TCTGTTCTCC GTCNAACTCA CCANANTCNA	720
	ACCTAACCCC NTNCNCTTCC NGGGTTCTCC TTNATGCACT NTGCNCCTAT TTNTTTCCCA	780
	ANGC	784

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 817 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

	CGGCACGAGA TATGGAGGTA TGATCGGGAG CTA CTGGGAG CTCCGCTTTG GTGAACAACA	60
	CGACGGCAAG AAGGGCTATG GATTCAAGGA GTGAAGGCCA TGGTACCGCA NAGGCGGGTC	120
	TTCCGGGCGT GCACCGAATT TTGCATCGGA TGAAACCTT GGTCATCAGC ATATGGGGGC	180
	TGGGTTCCAC CAAGGGAAAA GTTCGAATGC AAGTACCACT GAGTCCCATG AGAGGGACTT	240
	GATCATGCAG AGGTATGATC GAAGCAGCTG GAGANTTGGA CTGCTCCANA GCTCATATTC	300

5 GCTTAAGGGA GCCCGACAAG TCAGAGGACA AGGTCGAGTA AGCGAACGTT GCTACCCAAA 360  
 ATCAAGCATC AGTTANAATG GAGGTGGACT CANAGGAGTG CCACGGAAGA CATCTCTACT 420  
 GATTGTGAAG GAAAGGGATA CAGAGGCGAA NCGACGGATA NTANGGCCAT GGGCATGGCA 480  
 GCGCCATGGT ACCGCANANG CGGGACTTCC GTGCAAGTCA TTGATCCCTT GCTCTCACGG 540  
 10 AGGGANANCG CTTGGTCCTG AAAGGGGCCN AAGAAGTGGA CATGCANANG CAATCTCCAA 600  
 TTACCGAAAC ANGGCTGAAG GGCANAAGCC NANAACTTC CTNAGAACGG TGTCACAAT 660  
 TTCTCATCNA NATANCCGTA ATTAANGACT TCCGGTCATG CNANAATNCC CNACCNANGA 720  
 15 ACCAANCAGG CNTACTTGTG CTGTNCTTTG CTACCCNNTG AATNGCGCCN GGTNATNGA 780  
 AAAACGTCC TTCCCAAGC AACCTCTNT CAAAAAN 817

20 (2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 837 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

30

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-U40

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TTTTTTTTTT TTTTTTTTGG GTATCAGGCA AAGATGGATA CTTCCAGGTT TGCTATTTAA 60  
 40 GAACCATAGT CAGTCTTATG AGGAGAGACC ATACGTAATA CAATCTTTAA GATGACAAAA 120  
 TCCATTCCCTA CCAATACAAT GACCAAGCGA AAGGTACAAG GATAACGGGC AAAAGACTAA 180  
 45 ATTGCAACTA TATAAAATTC TGCTGCATTG TAGTAAATTC AACTGTGACG ACACGCCACC 240  
 AGGATGAAGT CTATCTATAA ACCCACTTAT TGCTAGATGG ACGGTGTAAC AGAGCTAAAA 300  
 CAGCAAAGTA GAATAAAGA AACTGACAAC GCTTCCGCAT GCGCTCCACA TATGGAGCCA 360  
 50 GGCGGAGGTT GGGCAATTGG AGGAAATGAC NTTTCTGACG GTGTAACATA AAANAATTT 420  
 GTAACACCGT CAAGTACGAT TTCCCATCCT TCGGGTTGTG GCGTTCTGCT ACTTGGCATT 480  
 55 ACGTTAACAT CGAGTGCCGA CTTGGCAAGA CAGGACCCCA GCATCAGAAG TCAGTGTGTC 540  
 AACCAAGGAA GAAGGCTTGG CCCCAAAGCT GGAGGCCCGT GCGTAACTGG CTGAACCCCT 600  
 GCACCGGAAN GGGTGAAAAA AGCACCATTC AGAACAGGTC NCCTCCGACC TCCCAATTCC 660  
 60 AGTTCTTCCA CCNTGCTTTT GATCTGTGTC CACCTTTTTG TTACCTATTC CATCGAAGCN 720  
 TANGGATTTT TAAAAATCCC GAAGGAAAGG AANTTCNAT AATTGGTGCN CCAANAAGG 780  
 AAGATGGACN GAACTGTGTG TGGTTGCTCC TGTTCTCCTT TTGCAATGGA TTGGTCG 837

65

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 799 base pairs  
 70 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

5

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-U108

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GGCACGAGGC AGCTCAATCG ACCGACTCCT CCTCCTCCTC CTCCTCCTCC TCTTGTCTT	60
15 CTATTCTAA TATAATTATC GCTTTTGGTG TGTACATCTT CTATAATTG AGAGGATGGA	120
GGCAGGATTG ATGGCGAAAC AAGCAGCAGC GGTGCGAAG CCGAACGCGT TCCCCGCCCCG	180
20 GAGCCTAGGG TTCGGGAGCT CGGTCAGGGG CGGATCCGGG ACCAGCAGGA TCGGGTTCGA	240
GGCGCCCGCG AGCGTGGCAT GGAGGAAGCG GTCGATTCAG GTGGCCCGCC AAGGAGCCAT	300
TCGGTCGGAG GTGGTCGTGG AANANAAAGC ATCNCCGCC AAAAAGGATA AGGCCGGTCC	360
25 GGGTCGGCTC TACGTGGGTC TGCCCTTGA CGTGGTCTCC GACGGCAACG TCNTCAACCA	420
CGGCAAGGCC ATCGCCCGCG GTCTCCGCGC CCTCCGCCCT CTCGGCGTT GATGGANTCN	480
AACTCCCCCA TCTCCTGGGG CGTTGGCGAT GGAATCCGGC GAATGGTCCT CCTACCTCCC	540
30 CCGTCNCCGC CATGGCGCGC GACNCCGGC CTTGCGCTCC GCGTCTCCCT CCACCTCCAC	600
TGCCANCGCC GCCCTCGCCT CCCCCTCCC NAATCGGTCG AATCCNCCGC CGCTAACAAA	660
35 CCCCAGAAATC CTATTCTCTG AACGCNCCGG CCGCCNCCNG TTGCCCAAAN TNGCCTTNTT	720
CCTTTCNCT TTGTTTNAAG AAAAATCCC CNTTGTTCCT TCCAANCGGG NAGGAACCCC	780
CNAATGGAAA CCTTNCAA	799

40

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 786 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

45

(ii) MOLECULE TYPE: cDNA

50

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-U128

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GGCACGAGGA AACGTCTCTC CCTCTCTCCA CTTCTCACAC CCCC GCCCCC GACTCAGCGA	60
60 ATCGACATTC TTGGCGTGTC AAGGAAACCT TTCTTTTATT TGCGAAGGAA CATGAGCAAT	120
ACTGTTGGAC ACACCTTACC CCAGCAAGCT CTTTACCGGC CTTCTATCAA AGAAAATCAA	180
65 AGTAAAGCTC ATCAAGGAGT TTCTGCAAAC TTCTGTGTG GAGTTCCATT AGGATCTAAG	240
GTGGAAAATG CAGTGTCATA CAGCTCTAGG TCACTGCTTT CAACCGGATC CCTGGGAAAG	300
AAACTCATCA AAGGAATC ACCAAAGCAA AATCCAAGCA TAGTCACTAT GACCCCTCGT	360
70 GCTGTGTTGG CTGCANATCC TGCTTCAGAG CTAAGGAGAA AATTCAAGCT TGACACAAAT	420

TCTGAATTGG AGGTTGTTGT TCATGTCCCT ACTTCGGGGT CTCCTGTNCA GATTGAATTT 480  
 CAAGTNACTA ACAGCAGTGG CTA CTCTGGTG CTTCNTTGGG GTGCAATTCA TAATANAAGG 540  
 5 AATAACTGGT CACTTCCTTC TCGTCATCCT GATGGAACAA AAGTTTNCCN AAACCCGAAC 600  
 TCTCANGANA CCTTTTAAAA AATCTGGTTC CCCATCNTCC GTNAAAATGG AGATTGATGA 660  
 10 TCCTGAAATA CCAGCAGTNG AATTTCTCCT TANTTTTGNA ACAAATNCTC AAAAAAACCN 720  
 AAATTGGGTT TTTAAACNA TTAATGGGTC CCNAAATTC CNTGTTCCNN TTTTTTTANA 780  
 AACAAAG 786  
 15

## (2) INFORMATION FOR SEQ ID NO: 40:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 804 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

25

## (vii) IMMEDIATE SOURCE:

(B) CLONE: U-D4

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

GGCACGAGAG ATAGCTGAAG TGACGTGAGG TGACTTCGAT TAGATCGAGA GAAATTTCTT 60  
 35 TGTGATTTTT GTGGACAATT CTCAATGGCT GCTGTAACAA ANTCACAATT CATCTCGAAA 120  
 GGCTCATGCG CTGGCTATGG GGGTGTGCTC GACTCGGAGC CAAGGACCTT CCTAAACAGA 180  
 40 AGGGTTCTAC ACTTGAGGAA CCAAACCACC GCTTACGAAG GATTGAGATC TCGAAATGTG 240  
 GTTGATTTGA TTCAGATGCC GTCTAATGCC AAGGTGATTT CAAGGAAAAC TGTGAGGGGA 300  
 ACTCAGAATC CTAGTCGTAN ACCTTGGGCT GTTGTCATTT GTGGAAAAGG GATGAACATA 360  
 45 GTCTTTGTCG GCGCTGANAT GGCTCCCTGG AGTAAAACCG GANGGACTCG GTGATGTTCT 420  
 TGGAGGACTG CCACCGGCCA TGGCTGCAAA TGGACACAGA NTGATGACTA TAGCTCCACC 480  
 50 CTATGATCAG TACAAGGATG GGTGGGATAC AAATGTCCTG GCTGAATTAA AAGTTGGAAA 540  
 TGAAATTGAA ANAATCCGCT TTCTTCCACT GCTATAAAAA AAGAATTGAC AGGGTTTTCA 600  
 TTGATCACCT TTGTTTCTTG AAAANGTGTT GGGAAAAACT GGAAGAATGA AATTTTGGTC 660  
 55 CTNTCCCCGG AACTGATTTT NAAAAACANC CCCTAAANTT TANCCTTTN TNCCNGCCN 720  
 CTTTGGAAA CTCCNGGAT NCTGGTTTTT TNCCACCCCC NAAAANTTTC CTNGAACCTN 780  
 60 TGGGGGAAAN TTTTTTTTTT TTTT 804

## (2) INFORMATION FOR SEQ ID NO: 41:

## (i) SEQUENCE CHARACTERISTICS:

65 (A) LENGTH: 826 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

70

## (ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-D10

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

10	GGCACGAGAG ATAGCTGAAG TGACGTGAGT GGACAATTCT CAATGGCTGC TGTAACAAAG	60
	TCACAATTCA TCTCGAAAGG CTCATGCGCT GGCTATGGGG GTGTCGTCGA CTCTGAGCCA	120
	AGGACCTTCC TAAACAGAAG GGTTCACAC TTGAGGAACC AAACCACCGC TTACGAAGGA	180
15	TTGAGATCTC GAAATGTGGT TGATTGATT CAGATGCCGT CTAATGCCAA GGTGATTTCG	240
	AGGAAACTG TGAGGGGAAC TCAGAATCCT AGTCGTANAC CTTGGGCTGT TGTCATTGTG	300
20	GGAAAAGGGA TGAACATAGT CTTGTGCGG GCTGANATGG CTCCCTGGAG TAAAACCGGA	360
	GGACTCGGTG ATGTTCTTGG AGGACTGCCA CCGGCCATGG CTGCAAATGG ACACAGAAGT	420
	GATGACTATA GCTCCACGCT ATGATCAGTA CAAGGATGGG TGGGATACAA ATGTCCTGGC	480
25	TGANTTAAAA GTTGGAATG AAATTGAAAG AATCCGCTTC TTCCACTGCT ATNAAANAAG	540
	AATTGACAGG GTTTTCATTG ATCATCCTTT GTTTTCTTGA AAANGTGTG GGAAAACTG	600
	GANGAATGAT ATNTGGTCCT GTCCCNCGAA CGGATTATTN AAAACCACCC NCTTAANATT	660
30	TACCCTTTTG TGCCCGANGCA NCNTTGGAA NCTCCAAGG ATTCTGGATN TTTAACNACN	720
	NCCNAATACT TTTCTGGAA CCATTTNGGG GANAANNTTG TTNTTGTG CNAATTAATT	780
35	GGCNCCTGG TCCTCCTNCC TGCTACTTAA AAATTTTNTT TCNTNT	826

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 813 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-D13

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

55	GGCACGAGCT GAGGGAGTGA GGGAAAGAGA TAGCTGAAGT GACGTGAGGT GACTTCGATT	60
	AGATCGAGAG AAATTTCTTT GTGATTTTGG TGGACAATTC TCAATGGCTG CTGTAACAAA	120
	GTCACAATTC ATCTCGAAAG GCTCATGCGC TGGCTATGGG GGTGTCGTCG ACTCGGAGCC	180
60	AAGGACCTTC CTAAACAGAA GGGTTCACAC CTTGAGGAAC CAAACCACCG CTTACGAAGG	240
	ATTGAGATCT CGAAATGTGG TTGATTGAT TCAGATGCCG TCTAATGCCA AGGTGATTTT	300
65	AAGGGAAAAC TGTGAGGGGA ACTCAGAATC CTAGTCGTAG ACCTTGGGCT GTTGTCATTT	360
	GTGGAAAAGG GATGAACATA GTCTTTGTG GCGCTGANAT GGCTCCCTGG GAGTAAAC	420
	GGAGGACTCG GTGATGTTCT TGGAGGACTG CCACCGGGCC ATGGCTGCAA ATGGACACAG	480
70	AAGTGATGAC TATAGCTCCA CGCTATGATC AGTACAAGGA TGGGTGGGAT NCAATGTCC	540

TGGCTGAATT AAAAGTTGGG AAATGAANTT GAAAGAATCC GCTTCTTCCA CTGCTATAAA 600  
 ANAAGAATTG ACAGGGTTTT CATTGATCAC CTTTGTCTT GAAAAGGTGT GGGGAAAAAC 660  
 5 TGAAGAATG ATATTTGGTC CTGTCCCNCG ACTGATTNA AACACCACC TAAAATTACC 720  
 TTTTGTNCCN GCNNCTTTGG AACCNCCCNG GATCTNGATN TTANACCCCC CAANTCTTAT 780  
 10 CCTGGAACCT TTGGGGNAAA NTTTGTNTTT GTT 813

## (2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:  
 15 (A) LENGTH: 805 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 25 (B) CLONE: U-D66

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

30 GGCACGAGAA GAGATAGCTG AAGTGACGTG AGTGGACAAT TCTCAATGGC TGCTGTAACA 60  
 AAGTCACAAT TCATCTCGAA AGGCTCATGC GCTGGCTATG GGGGTGTCGT CGACTCGGAG 120  
 35 CCAAGGACCT TCCTAAACAG AAGGGTTCTA CACTTGAGGA ACCANACCAC CGCTTACGAA 180  
 GGATTGANAT CTCGAAATGT GGTGATTTG ATTCAGATGC CGTCTAATGC CAAGGTGATT 240  
 TCAAGGAAAA CTGTGAGGGG AACTCACAAT CCTAGTCGTA NACCTTGGGC TGTGTGTCATT 300  
 40 TGTGGAAAAG GGATGAACAT AGTCTTTGTC GGCCTGAGA TGGCTCCCTG GANTAAAACC 360  
 GGAGGACTCG GTGATGTTCT TGGAGGACTG CCACCGGCCA TGGCTGCAA TGGACACACA 420  
 45 GTGATGACTA TAGCTCCACG CTATGATCAG TACAAGGATG GGTGGGATAC AAATGTCCTG 480  
 GCTGANTTAA AANTTGGAAA TGAAATTGAA AAGANTCCGC TTCTTCCACT GCTATAAAAN 540  
 AAGAATTGAC AGGGTTTTCA TTGATCATCC TTTGTTTCTT GAAAAAGTGT GGGGAAAAAC 600  
 50 TGGGAAGAAT GATATNTGGT CCTGTCCCNCG GAACTGATTA TAAAACACCA GCTAANATTA 660  
 CCTTTTGTG CCAGCAACTT TGGAACCCCN AGGATTCTGG ATNTTACAAC ACNAATACTA 720  
 55 TTCTGGAACA TTTGGGGAAA AATTGTTTTT GTTNCCAATG ANTGGCNCAC TGGTCCCNCT 780  
 CCTNCCTACT TAAAAANTTT TTTCC 805

## (2) INFORMATION FOR SEQ ID NO: 44:

60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 790 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

65 (ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 70 (B) CLONE: U-D111

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

5  GGCACGAGAA GAGATAGCTG AAGTGACGTG AGTGGACAAT TCTCAATGGC TGCTGTAACA      60
   AAGTCACAAT TCATCTCGAA AGGCTCATGC GCTGGCTATG GGGGTGTCGT CGACTCTGAG      120
10  CCAAGGACCT TCCTAAACAG AAGGGTTCTA CACTTGAGGA ACCAAACCAC CGCTTACGAA      180
   GGATTGAGAT CTCGAAATGT GGTTGATTTG ATTCAGATGC CGTCTAATGC CAAGGTGATT      240
   TCGAGGAAAA CTGTGAGGGG AACTCAGAAT CCTAGTCGTA GACCTTGGGC TGTGTGCATT      300
15  TGTGGAAAAG GGATGAACAT AGTCTTTGTC GGCCTGANA TGGCTCCCTG GAGTAAAACC      360
   GGAGGACTCG GTGATGTTCT TGGAGGACTG CCACCGGCCA TGGCTGCAA TGGACACAGA      420
   GTGATGACTA TAGCTCCACG CTATGATCAG TACAAGGATG GGTGGGATAC AAATGTCCTG      480
20  GCTGAGTTAA AAGTTGGAAA TGAAATTGAA AGANTCCGCT TCTTCCACTG CTATAAAAGA      540
   AGANTTGACA GGGTTTTTCAT TGATCATCCT TTGTTTCTTG ANAAGGTGTG GGGAAAAACT      600
25  GGAAGAATGA TATATGGTCC CTGTCNCAGG AACNGATTAT GAANACAACC AGCTAAGATT      660
   AACCTTTTGT TGCCAGCACT TTGGGAACCN CAAGGATCCT GGATCTTAAC AACNCAANTC      720
   TATTCTGGAC CATATGGGGA CAAATTGTTT TGTGCAAAT GATGGCACCT GTCCNNTCC      780
30  ATGCTACTTA                                     790

```

## (2) INFORMATION FOR SEQ ID NO: 45:

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35  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 813 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: unknown

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40  (ii) MOLECULE TYPE: cDNA

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45  (vii) IMMEDIATE SOURCE:
      (B) CLONE: U-D112

```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

50  TTTTTTTTTT TTTTTTTT GAGCATAATA GCAATTTATT CAGGAGGATC AAACCTCAAAC      60
   ACTATAACAT AGACAGTAGT CACTTTCAGG GAGTGGCCAC ATTTTCCTTT GCAAGAGGAG      120
55  CTATTTTCATC AGCATCGATG CCGGCTTCAC TACCAGCAGC TCCTAAGCTT AGGANAAATT      180
   GCTCCCACTT CTTAGCAGGT CCCTTCCAGG AGAGGTCTTG AGTCATGCAG TTCTGTATCA      240
   TCTCAGCAAA TGCAGGTGTG CCGTAAACTT TAAGGGCCCT TTTCAGTGTG TGAATGACTT      300
60  TTTGTACATC ATCTTTATCG ACAACATCAC AATCAGGATT GAAGGGACCC ATATGAAACC      360
   CTGTGATGCC TTCTATGACA GTGTCAGCAA GTCCACCAGT TGTGCGCAC ATGGGGGGAA      420
65  TTCCATATCG CATGCCCTGA AAGCTGGATA AGGCCACAAG GTTCGAATCT GCTGGTAAGA      480
   NCAAGAAGAT CTGCTCCAGC CATGATTTCA TGANCCAAAG GTGCATTAAA CTTCATATGT      540
   GCTCTCACTT TATTGGGAAA CATATCTTCA AGTTGTGCAA GCTGACGCTC CAACANCTTC      600
70  TCCCANTACC AAGCACTATC ACTTGAACAT TTTATCAAT GAATTCAGGA ATAAGTGCNG      660

```



CGAAAAATATC CGAACCTTTC TGCTCTCTAA TCTCCCTATA AAGGNTATAA CAGGGATTTC 720  
 5 CNGTCAACAG GTTAACCAAA TTCAACTTGT TAGGNTTCCC TTAATCCAAA GGTTCGACC 780  
 CNNCCCATTG GTTGCTCNTA ATTGANAAAA ATT 813

## (2) INFORMATION FOR SEQ ID NO: 46:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 808 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

20 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-D39

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

25 GGCACGAGCG AGTTTTTTTT TTTTTTTTTT GCTGTGATGA TATTATGCAT CTTATTAGTT 60  
 GGTTCACCA CTTCTATTAC ATCACTCAAC AGTATTAGCC CAAGANAAGG CTAATACCTT 120  
 30 CNCATCACTC TTGACATCTT ATTTGTATTG TAGGANACTA GTATATATAT CTATATGCGT 180  
 GGTTCCTGC ACNAGGGCGG CTTATTAGTG GCGTCAGTGA TCTCAAGGGC AGAANACAAC 240  
 35 CCTGTANTTG GTGCCGCCGG GGCAGGTGAA GGTGCTCGTC TGATCGTCCT TGGGATANCT 300  
 GTAGGCGTCG GGGCAGTTTC TCTTGAANAA CCGGGAGTAT TCGGTCGGGC TGCAGCTGCC 360  
 GGAGTTGCAA CAGTACTGGT CCGTCTTGAA CACGGTGCAG GGGTTGTTGC ANCCGCCCGG 420  
 40 CGCCTTCANC GCCCCGGGGC ACTGCCCGTT GATNTCCGCC GCGCACCGBA TGCCGCGGCA 480  
 NCCGCCTGAC NTGGGGCTNA ATCCCATTGG CACGTTGAAA CCGTCNACCA AGGGAAATTT 540  
 45 CAAAAAATCC AAGTTGTTGA ACTGGTTGAA CGCCAACTCC NCCAGGGTNT TGGGCCGGTT 600  
 GCCNTACCCC GTGCATNACA ACACCCCGCC GCANTCCCT TCTGGCACCG CCGCNTCCGC 660  
 TCCCCTCAA AGAACACCCG TGCGGCCCAA AATCCGGNCC CCCGGTGGTT CCCCCTTTCN 720  
 50 CTTTAANGGT CCCCAATGCC CCTGNTTTAA CTGNCTCCCC CCCANGCNCG GCCCCGGCCC 780  
 ACNCTTTNTT AAAACATCNG TNCCNAAT 808

## (2) INFORMATION FOR SEQ ID NO: 47:

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 809 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 60 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

65 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-D50

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

	GGCACGAGTG TGCCTAACAG AGAAAGAGAG ACCGATAGCC TCCTCATTCA CTATGGCGAT	60
	CCGATCGCCA GCTTCGCTGC TGTATTGTC GTTCTGATG CTTGCGCTCA CAGGAAGACT	120
5	GCAGGCCGGG CGCAGCTCGT GCATTGGCGT CTAAGGGGA CAAAACACAG ACGAGGGAAG	180
	CTTAGCAGAT GCTTGTGCCA CAGGCAACTA CGAATACGTG AACATCGCCA CCCTTTTCAA	240
10	GTTTGGCATG GGCCAACTC CANAGATCAA CCTCGCCGGC CACTGTGACC CTCGGAACAA	300
	CGGCTGCGCG CGCTTAAGCA GAGAAATCCA GTCCTGCCAG GAGCGTGGAG TCACGGTGAT	360
	GCTCTCCATC GGAGGTGGCG GGTCTTATGG CCTGAGTTCC ACCGAAGACG CCAAGGACGT	420
15	GGCGTCATAC CTCTGGCACA GTTCTTGGG TGGTCTGCT GCTCGCTACT CTCGACCCCT	480
	CGGGGATGCG GTTCTGGATG GCATANACTT CAACATCNCC GGAGGGAGCA CAGAACACTA	540
20	TGATGAACTT GCCGCTTTC TCAAGGGCTA CNACGAACAG GAAGCCGGAA CGAAAAAANT	600
	TTTACTTGAA TGCTGCTCCC NCANTGTCCT TTCCCGGATT ACTGGCTTGG CACCCACTCA	660
	NAAAAATCT CTTCNACTT CCNTGTGGGT TGCANTTCCT CCAANAACCC TTCCTTGCCN	720
25	TTTCTCCCCA AAACCTATCC ATCTTGCAAT TCCTTTCACA AATTGGGTCN TNTCNTCCC	780
	NGCCCCNAAA ACTTTTTCCT TNGGGCTCC	809
30	(2) INFORMATION FOR SEQ ID NO: 48:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 809 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	
40	(vii) IMMEDIATE SOURCE:	
	(B) CLONE: U-D86	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:	
	GGCAGAGCC ACAAGCTTGC CTTTGGTTGT GCCTAACAGA GAGAGAGAGA GAGACAGACC	60
50	GATAGCCTCC TCATTCACTA TGGCGATCCG ATCGCCAGCT TCGCTGCTGT TATTTGCGTT	120
	TCTGATGCTT GCGCTCACAG GAAGACTGCA GGCCCGGCGC AACTCATGCA TTGGCGTCTA	180
	CTGGGGACAA AAGACAGACG AGGGAAGCTT AGCAGATGCT TGTGCCACAG GCAACTACGA	240
55	ATACGTGAAC ATCGCCACCC TTTTCAAGTT TGGCATGGGC CAACTCCAG AGATCAACCT	300
	CGTAGCCAC TGTGACCCTC AGAACAACGG CTGCGCGCGC TTAAGCAGCG AAATCCAGTC	360
60	CTGCCAGGAG CGTGGAGTCA AGGTGATGCT CTCCATCGGA GGTGGCGGGT CTTATGGCCT	420
	GAGTTCCACC GAAGACGCCA AGGACGTGGC GTCATACCTC TGGCACAGTT TCTTGGGTGG	480
	TTCTGCTGCT CGTACTCTC GACCCCTCGG GGATGCGGTT CTGGATGGCA TAACTTCAA	540
65	CATCNCCGGA GGGAGCACAG AACACTATGA TGAAGTTGCC GCTTTCCTCA AGGGCTACAA	600
	CGANCAGGAA GCCGGAACGA AAAAAGTTCA CTTGAATGCT GCTCCCCANT GTCTTTCCCG	660
70	GATTACTGGC TTGGCAACGC NCTCCAAAAC AAATCTCTTC CACTTCCTGT GGGTGCAATC	720
	CTCCACAAAC CTTNTGTCAT TCTCCCCAAA CCTATCAATC TTGCNAAATG CGTTCAACAA	780

TTNGGGTCTT TTCATCCCCG CCCAAAAC

809

## (2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 785 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
(B) CLONE: U-D90

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GGCAGGAGGA GAGACCGATA GCCTCCTCAT TCACTATGGC GATCCGATCG CCAGCTTCGC 60  
TGCTGTTATT TGCCTTTCTG ATGCTTGCGC TCACAGGAAG ACTGCAGGCC GGGCGCAGCT 120  
CGTGCAATTGG CGTCTACTGG GGACAAAACA CAGACGAGGG AAGCTTAGCA GATGCTTGTG 180  
CCACAGGCAA CTACGAATAC GTGAACATCG CCACCTTTT CAAGTTTGGC ATGGGCCAAA 240  
CTCCAGAGAT CAACCTCGCC GGCCACTGTG ACCCTCGGAA CAACGGCTGC GCGCGCTTAA 300  
GCAGAGAAAT CCAGTCCTGC CAGGAGCGTG GAGTCACGGT GATGCTCTCC ATCGGAGGTG 360  
GCGGGTCTTA TGGCCTGAGT TCCACCGAAG ACGCCAAGGA CGTGGCGTCA TACCTCTGGC 420  
ACAGTTTCTT GGGTGGTTCT GCTGCTCGCT ACTCTCGACC CCTCGGGGAT GCGGTTCTGG 480  
ATGGCATANA CTTCAACATC GCCGGAGGGA GCACAGAACA CTATGATGAA CTTGCCGCTT 540  
TCCTCAAGGC CTACAACGAG CAGGAAGCCG GAACGAAAAA AGTTTACTTG AATTGCTGCT 600  
CCGCANTATC CTTTCCNGAT TACTGGCTTG GCAACNCNCT CCAAAAAANA TCTCTCCAC 660  
TTCCTGTTGG GTGCAGTTCT TCCAANAACC CNTTCNTGCC ATTTCTCCCC AAAACGCTTT 720  
CCATCTTTGC AAATGCCTTT CAACAATTGG GGTCTGTTC CNNCCCTGCC CAAAAAACTG 780  
TTCCT 785

## (2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 813 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
(B) CLONE: U-D93

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

GGCAGGAGCG ATAGCCTCCT CATTCATAT GGCGATCCGA TCGCCAACCT CGCTGCTGTT 60  
ATTTGCGTTC CTGATGCTTG CGCTCACGGG AAGACTGCAG GCCCGGCCCA GTCATGCAT 120

	TGGCGTCTAC TGGGGACAAA ACACCGACGA GGGGAAGCTTA GCAGATGCTT GTGCCACAGG	180
	CAACTACGAT TACGTGAACA TCGCCACCCT TTTCAAGTTT GGCATGGGCC AAACCTCCAGA	240
5	GATCAACCTC GCCGGCCACT GTGACCCTCG GAACAACGGC TGCGCGCGCT TGAGCAGCGA	300
	AATCCAGTCC TGCCAGGAGC GTGGCGTCAA GGTGATGCTC TCCATCGGAG GTGGCGGGTC	360
10	TTATGGCCTG AGTTCCACCG AAGACGCCAA GGGGAAGTAGC GTCATACCTC TGGCACAGTT	420
	TCTTGGGTGG TTCTGCTGCT CGCTACTCGA GACCCCTCGG GGATGCGGAA CTGGATGGCA	480
	TANACTTCAA CATCGCCGGA GGGAGAACAG AACACTATGA TGAACCTGCC GCTTTCTCTCA	540
15	AGGCCTACAA CGANCAGGAA GCCGGAACNA AAAAAGTTCA CTTGAATTGC TGCTCCGCAG	600
	TGTCCTTTCC CGGATTACTG GCTTGGCAAC GCACTCAGAA CANATCTCTT CNACTTCCTG	660
20	TGGGTGCAAT TTCCTCCACA ANCCTTCNT GCCATTTCTC CCAAAAAGCT ATCNATCTTG	720
	CAAATGCGTT CNACAATTGG GTCTTTTCCA NCCTGCNCAA AACTGTTCTT TGGGCTCCCC	780
	CTGCCCCCTGA AGGTGCNCCA ATTGGTGGCT NCT	813
25	(2) INFORMATION FOR SEQ ID NO: 51:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 819 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	
35	(vii) IMMEDIATE SOURCE:	
	(B) CLONE: U-D61	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:	
	GGCACTCAGG AACTCCAACA TCCAAGTCCT GTTGGATGTC CCCCATCCG ACGTGCAGTC	60
45	ACTGGCCTCC AATCCTTCGG CCGCCGGCGA CTGGATCCGG AGGAACGTCG TCGCCTACTG	120
	CCCCAGCGTC TCCTTTTCGAT ACATAGCTGT CGGAAACGAG CTGATCCCCG GATCGGATCT	180
50	GGCGCAGTAC ATCCTCCCCG CCATGCGCAA CATCTACAAT GCTTTGTCCT CGGCTGGCCT	240
	GCAAAACCAG ATCAAGGTCT CGACCGCGGT CGACACGGGC GTCCTCGGCA CGTCCTACCC	300
	TCCCTCCGCC GGCGCCTTCT CCTCCGCCGC CCAGGCGTAC CTGAGCCCCA TCGTGCAGTT	360
55	CTTGGCGAGT AACGGAGCGC CGCTCCTGGT CAATGTGTAC CCTTATTTTA GCTACACCGG	420
	CAACCCGGGA CAGATCTCGC TGCCCTACGC CCTGTTACAG GCCTCCGGCG TCGTCGTGCA	480
60	GGATGGGCGA TTCANCTATC AGAACCTGTT CGACGCCATC GTCGACGCGG TCTTCGCGGC	540
	GCCTGGAAAA AATGGGAAGG GCGAACGTGG CGGTGGTGGT GTCCGAAAAC GGGTGGCCGT	600
	CCGCGGGCGG AAGAACCNA AACNAACACC ANCAACNCG CCGGAANTTT CAACCANAAC	660
65	TTGATCAGGC ATGTTNGGCG GAAGAACCCC AAGGAAAACC AGGGAAGGAA ATCAAGGCTT	720
	CNTNTTCCAA AANTTTCCAC CAAAAACCNA AAGGTGGANG GATCCAACAA AACTTTGGCC	780
70	TGTTTTATCC CAANNAACAN CCCNTCTTAC CNAATAACT	819
	(2) INFORMATION FOR SEQ ID NO: 52:	

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 794 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
(B) CLONE: U-D63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GGCACGAGGG ATTATAAAAA GAAACTCGCA CTCAGCCAGA TTGACTCAAG CATGAAGGTT 60  
GCATCTTTTCG AATGTTCTTT TTTTTCCTCA CATCTTTTGA ATGTTACATG ACAATCATGA 120  
CGCCGTGCAT ACAATGATAC CTCTGATAGG GTTGAATGCA CAAACCACTC ATCGTGCTAT 180  
ATTGCAAGTG CTTATGTTTG TATTCATTTT CTTATAATTT CAATGTGAGA GTTACCTTAG 240  
GTTTCATATTA NATTTATATA ATATTGGGCA TAGATTTTTT TGTCATTGTT TGTGATCTGC 300  
AATTTTCATTA GGTCATCGAC CATATTATGG TAAATTTAAT TTACTAAATT ATATCTTGAG 360  
TTTATTGCTT TGCATATTTT GTGCTGGAAA CCATGCCAAT CCAACTCCTT TGCAAACTT 420  
AAGATAATTA AAGGAGATAT TGAGGATGCC GACTGCTTTA GGTTATTTGC ATTANACAAT 480  
AAACGCCCGT GAAATGGAAA TCATGCAAAG CTTTGCATGG AGAATATGTT NATAGAGATA 540  
GACATGAAGA CATGAATATG CTTTCTTGAT GAACAACGAT GTTACACNTGT TTACTGCATG 600  
CATGATACAT CCAATGTTCT AGGCTTGTTG GCAATCATTT TATTCNAAAA ATTGTCTGTT 660  
TCTCTNCCNC CATAAGGTTA GCTTGTGGAA AATGTTCAAC TTTGGGCNCA NATGATCCGT 720  
TTTAGCAAAA TCCCNCCATT CCTATTTTTT TCCGGAATCC NNTTGGNAAA ANATCCTNAC 780  
ATACTATTTT CACA 794

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 798 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
(B) CLONE: U-D65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGCACGAGGC CCGTAGAGCG AGTGCTGAGA TGGCTTTGAG GGCCTTCTTC CCCCTCTGCA 60  
TCGCTCTCGT GGTGACGCTC TCACCTCTGT GTGATGCCAC TTCGCCTTAC TACACCATCA 120  
CACCGCCAC CCGGTGGCC AAGCCGCCTT CAGTTGAACC ACCACCCTAC CACGCGCCTC 180  
CGACGACCCA CCCTAAGCCA CCGAGTCATG GTGGCCAACC TCCGTCCCAC CATCACCCAA 240

CACCAATCTA CGGTGCACCC CCTCCGCAAC ACCACCACCA CCACCAACAC CACCACCAAC 300  
 CTGCACCACC AACTCAGCA GAACACCCTC CGTACTACCA CATGCCTTCC CCGCCGCCGC 360  
 5 ATGGCCAGCA CCCGTCACCA CCGTCACATG ATTATCCCGT ACCTCCTGCT CACAAGCCCC 420  
 GAACTCCGCC GCCGGTTTAC AAGTCTCCAC CACCGACCCA CCGTCCTTAC CCTCCATCGA 480  
 CGCCACCCCA CCATCCGACG CACCCGCCTT CTCAGCCGAC GCCGTCATAC AAGGCCCCGC 540  
 10 CACCATACAA GAACATCCCT GANCATCTCC ACCGCCGCGT CACTATCATT CTCCGTCTTC 600  
 ACCACCANCA CAACCACCAT NCAATAGTC TCGTTTGCAT CTCTCCGTTG AANATGAACC 660  
 15 AATGTCNTTT AATAACGATC AGGGTTTCAA ATAAAAACNA ATTTCCGCCA TTGTAATGCT 720  
 ATGGTTGTTC TCTCTGCTTC CCGGGGAAAG TTTCTTGGGT CATNTTAACC NCCTCCTAAT 780  
 GTTCNGCTCT TNNTANAA 798

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: U-D84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GGCACGAGCG CCCACCCCGG TGGCCAAGCC GCCTTCAGTT GAACCACCAC CCTACCACGG 60  
 40 CCCTCCGACG ACCCACCCTA AGCCACCGAG TCATGGTGGC CAACCTCCGT CCCACCATCA 120  
 CCCAACACCA ATCTACGGTG CACCCCTCC GCAACACCAC CACCACCACC AACACCACCA 180  
 45 CCAACCTGCA CCACCAACTC ACGCAGAACA CCCTCCGTAC TACCACATGC CTCCCCGCC 240  
 GCCGCATGGC CAGCACCCGT CACCACCGTC ACATGATTAT CCGGTACCTC CTGCTCACAA 300  
 GCCCCGAAGT CCGCCGCCGG TTTACAAGTC TCCACCACCG ACCCACCCTC CTTACCCTCC 360  
 50 ATCGACGCCA CCCCACCATC CGACGCACCC GCCTTCTCAG CCGACGCCGT CATACAAGGC 420  
 CCCGCCANCA TNCNAGACCA TCCCTTGAGC ACTTCTCCAN CGNTTGCGTT TATTATCATT 480  
 55 CTCCGTCTTC ACCACCACCA CCACCACCAT ACAAATAGTC TCGTTTGCCA TCTCTCCGTT 540  
 GAAGATGACG CAGTGTGCTT TTAGTAGCGA TCAGGGTTAC CAATAAGAAC GATGTTGCCG 600  
 CCATTGTAAT GGCTATGGTT GTTCTCTCTG CTTTCCGGG GGAAGGTTCT TTGGGTTTCA 660  
 60 GTTAAACCTC TCTCTTAAAT GTTCATGCAT CTTATTATAA ACNAAAATTG GCCATTTNNN 720  
 NNNNTNTNTN NNNNNTTNNN NNNNNAAAAC TCNAAAATA TTTTAAAAA CGGGCGGGGG 760  
 65 GCCCATCNAT TTTCCNNCCC GGGTNGGGGN TCCAGNTTA TTNT 824

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

5

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-D75

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

15	GGCACGAGGG TTACGATCGT CATGTTGGGG GTGTTACGCG GGNAGGTGG TGGAGGTGCC	60
	GGCGGAGCTG GTGGCCGCCG GCAGCAGGAC GCCGTCCCCT AAGACACGAG CGTCGGAGCT	120
	GATCAACCGA TTCCTCGGGA GCTTCGCTCC CGCGGTGTCG ATCCAGATCG GGGACTTGGG	180
20	ACACCTCGCC TACTCCCACG CCAACCAGTC CCCCTTCGCT CCCAGGTTGT TTGCAGCGAA	240
	GGACGANATT TACTGCCTCT TCAAGGGAGT GCTGACCAAC CTGGGCAGCT TGAGGCAGCA	300
	GTATGGGCTT TCCAAGAGTG CCGACNAGGT GGTGCTGGTC ATCGAAGCCT ACAAGGCCCT	360
25	CCGTGACCGA GCTCCCTATC CTCCCAGCTT CATGCTCGCA CACCTTACTG GCAACTTCGC	420
	CTTCGTGCTC TTCGACAAGT CCACATCATC CATCCTTGTT GCATCTGACC CANATGGAAN	480
30	ANTACCCTTG TTCTGGGGGA TCACTGCANA TGGATGCCTT GCCTTTGCTG ACNATCTANA	540
	CTTGCTGAAG GGATCGTGCG GGAAGTCACT TGCACCATTC CCTGAAGGAT GTTACTATTC	600
	CAATGCCTTG GGGGGCCTGA AAANCTATGA AAACCCCAAC ACAAGGTGAA CTGCTGTTTC	660
35	TTGAANATGA AGAANAATTN TTTGTGCCNC TTTCAAGGTG GAANGATCTG CCNTTCTTGC	720
	GGNAACCCCC TAATCAAGGA ACATCTTCCA ATGTTTGGGG CNAATGATCC TCTTAAAATC	780
40	CTAAAATTCT TGGAATT	797

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 804 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

45

(ii) MOLECULE TYPE: cDNA

50

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-D83

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

60	GGCACGAGCT TCCACACAGG TGAGGGTAAG TCGTTACGA TCGTCATGTT GGGGGTGTT	60
	AGCGGGGAGG TGGTGGAGGT GCCGGCGGAG CTGGTGGCCG CCGGCAGCAG GACGCCGTCC	120
	CCTAAGACAC GGGCGTCGGA GCTGATCAAC CGATTCTCG GGAGCTTCGC TCCCGCGGTG	180
65	TCGATCCAGA TCGGGGACTT GGGACACCTC GCCTACTCCC ACGCCAACCA GTCCCCCTTC	240
	GCTCCCAGGT TGTTTGCAGC GAAGGACGAN ATTTACTGCC TCTCAAGGG AGTGCTGACC	300
70	AACCTGGGCA GCTTGAGGCA GCAGTATGGG CTTTCCAAGA GTGCCGACNA GGTGGTGCTG	360

GTCATCGAAG CCTACAAGGC CCTCCGTGAC CGANCTCCCT ATCCTCCCAG CTTTCATGCTC 420  
 GCACACCTTA TTGGCAACTT CGCCTTCGTG CTCTTCGACA AGTCCACATC ATCCATCCTT 480  
 5 GTTTGTCATCT GACCCANATG GAAAAATGCC CTTGTTCTGG GGGATCACTG CANATGGATG 540  
 CCTTGCCTTT GCTGACNATC TANACTTGCT GAAGGGATCG TCGGGGAANT CACTTGCACA 600  
 10 TTCCCTGAAN GATGTTACTA TTCCAATGCC TTGGGGGGGC TGAAAANCTA TGAAAACCCA 660  
 ANCACAAGGT GACTGCTGTC TTGAANATAA AGAAAAATTT TTTGTGCCCC TTTCAAGGTT 720  
 GAANGATCTG CATTCTTGCG GCACCCCTN ATCNAGGAAC NTCNTNCCAA TGTGGGGCA 780  
 15 AATATCCTCT TAAAAANCAT AAAA 804

## (2) INFORMATION FOR SEQ ID NO: 57:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 803 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

25 (ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 30 (B) CLONE: U-D64

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

35 GGCACGAGGG ATTATAAAAA GAAACTCGCA CTCAGCCAGA TTGACTCAAG CATGAAGGTT 60  
 GCATCTTTTCG AATGTTCTT TTTTTTCCAA CATCTTTTGA ATGTTACATG ACAATCATGA 120  
 CGCCGTGCAT ACAATGATAC CTCTGATAGG GTTGAATGCA CAAACCACTC ATCGTGCTAT 180  
 40 ATTGCAAGTG CTTATGTTTG TATTCATTTT CTTATAATTT CAATGTGAGA GTTACCTTAG 240  
 GTTCATATTA GATTTATATA ATATTGGGCA TAGATTTTTT TGTCATTGTT TGTGATCTGC 300  
 45 AATTTCATTA GGTCATCGAC CATATTATGG TAAATTTAAT TTAATAAATT ATATCTTGAG 360  
 TTTATTGCTT TGCATATTTT GTGCTGAAA CCATGCCAAT CCAACTCCTT TGCAAAACTT 420  
 AAGATAATTA AAGGAGATAT TGAGGATGCC GACTGCTTTA GGTTATTTGC APTANACAAT 480  
 50 AAACGCCCGT GAAATGAAA TCATGCNAAG CTTTGCATGG AGAATATGTT NATAGANATA 540  
 GACATGAAGA CATGAATATG CTTTCTTGAT GAACAACGAA GTTCACNTGT TTAATGCATG 600  
 55 CATGATACAT CCAATGTTCT AGGCTTGTTA GGCAACCTTT ATCCAAAAAA TTGTCTGTAC 660  
 TCTCCCCCAT AAGGTAAGCC TGTGGAAAAT GTTCACTTTG GGCCNNATGA TCAGTTTANC 720  
 CGAAATCCC CCTTCNTTAT TTGTTTTCTG AAACNCNTTG GAAANANATT CCTTACATAC 780  
 60 CTTTTTCACN NANATNTTGA ACC 803



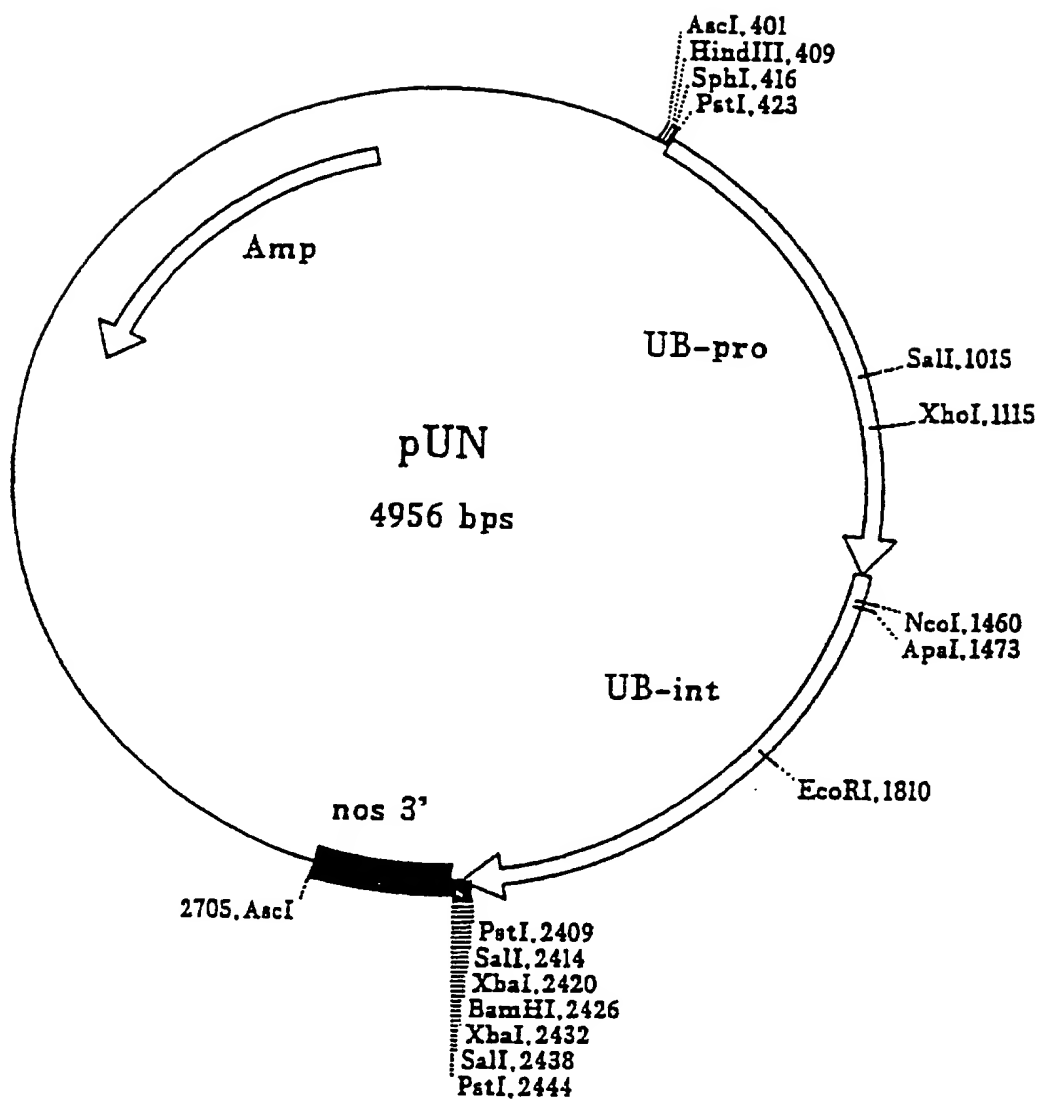
## CLAIMS

- 5 1. A method of modulating the ripening or tissue senescence process in plants of the genus *Musa* comprising inserting into plant material at least one polynucleotide sequence selected from the sequences depicted as SEQ ID Nos 1 -57, regenerating said plant material and selecting from the transformed regenerants, plants with modulated ripening or tissue senescence characteristics.
- 10 2. A method according to claim 1 wherein the polynucleotide is obtained from the cDNA library having the NCIMB Accession Number 40814.
- 15 3. A method of modulating the ripening or tissue senescence process in plants of the genus *Musa* comprising inserting into plant material at least one polynucleotide sequence or a fragment thereof, obtainable by hybridisation, from the cDNA library having the NCIMB Accession Number 40814, by the use of at least one of the sequences depicted as SEQ ID Nos 1-57 as oligonucleotide probes, said hybridisation being conducted at a temperature from 60°C to 65°C in 0.3 strength citrate buffered saline containing 0.1% SDS followed by rinsing at the same temperature with 0.3 strength citrate buffered saline containing 0.1% SDS, regenerating said plant material and selecting from the transformed regenerants, plants with modulated ripening or tissue senescence characteristics.
- 20 4. A method according to claim 1 or 2 or 3, characterised in that the said polynucleotide modulates the production of pectate lyase.
- 25 5. A method according to claim 4 in which the polynucleotide sequence comprises at least one of the sequences depicted in the sequence listings as SEQ ID Nos. 13-18.
- 30

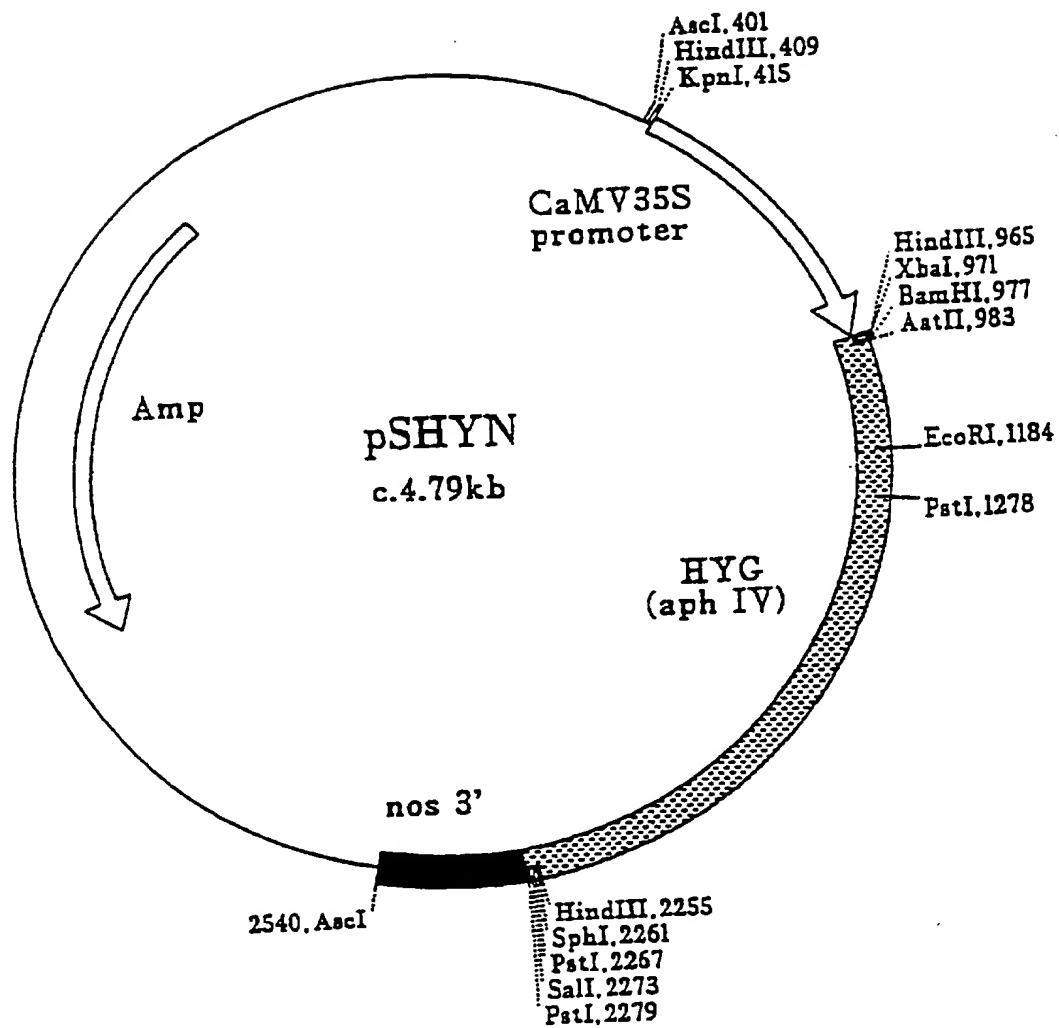
6. A method according to any preceding claim wherein the plant material is transformed using the *Agrobacterium*, microparticle bombardment, fibre mediated or direct insertion method.
- 5 7. Plants, their progeny and seed and material obtained from said plants, produced according to a method as claimed in claims 1 to 6.
8. A vector functional in plants comprising a promoter region which is operable in plant cells, a polynucleotide sequence defined in claims 1 to 3 and a transcription  
10 termination sequence.
9. A vector according to claim 8 wherein the promoter is constitutive, developmentally regulated or switchable.
- 15 10. A vector according to claim 9 wherein the promoter is tissue specific or organ specific.
11. A genetically modified banana produced via the method according to claims 1 to 6 having altered fruit characteristics when compared with a banana which is not  
20 transformed with at least one of the polynucleotide sequences described in claims 1 to 3.
12. A method of controlling plant pathogens comprising the application of an anti-pathogenic agent to plants, characterised in that plants to which the said agent is  
25 applied are plants according to claim 7.
13. A polynucleotide associated with fruit ripening selected from SEQ ID Nos. 1-57.
14. A fruit of a plant of the genus *Musa* having a retarded ripening phenotype generated  
30 by inserting into the genome of the said plant at least one of the polynucleotide(s) as claimed in claim 13.

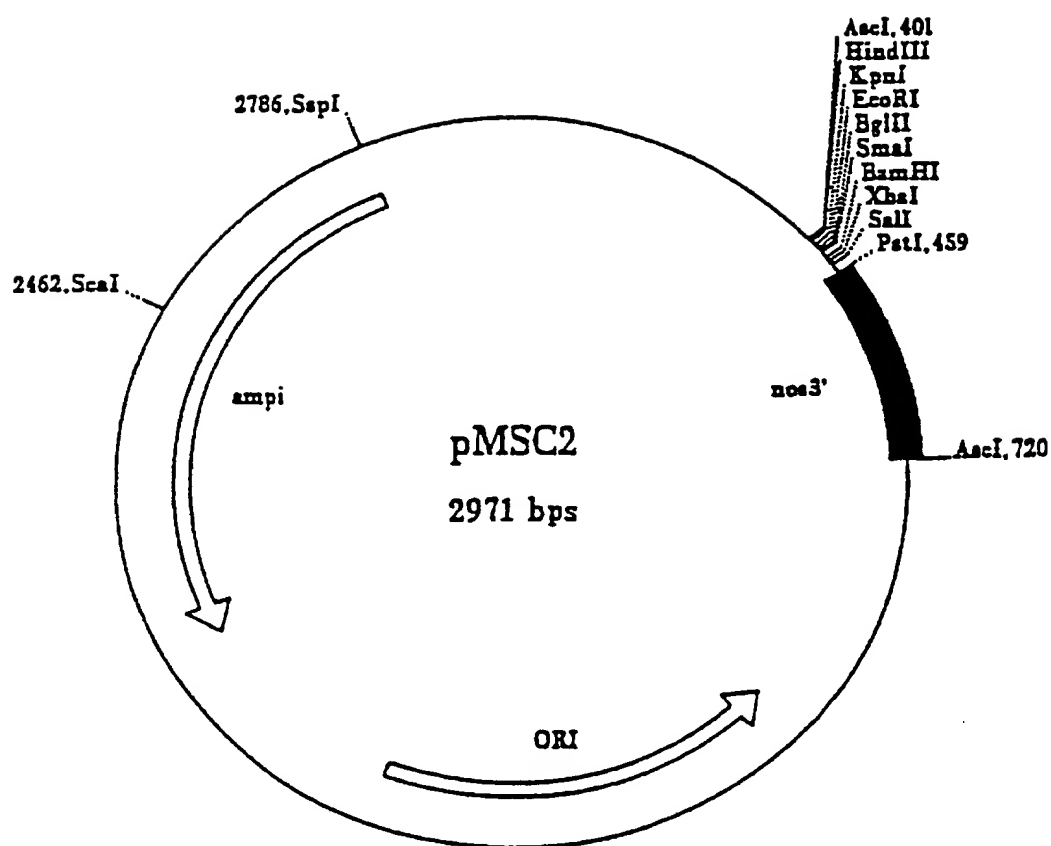
15. A method, polynucleotide, plant, its progeny, seed and material obtained from said plants and a banana substantially as hereinbefore described with reference to the accompanying drawings and figures.

1/3



2/3





BUDAPEST TREATY ON THE INTERNATIONAL  
RECOGNITION OF THE DEPOSIT OF MICROORGANISMS  
FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

Zeneca Limited,  
Jealott's Hill Research  
Station,  
Bracknell,  
Berkshire.  
RG12 6EY

VIABILITY STATEMENT  
issued pursuant to Rule 10.2 by the  
INTERNATIONAL DEPOSITARY AUTHORITY  
identified on the following page

NAME AND ADDRESS OF THE PARTY  
TO WHOM THE VIABILITY STATEMENT  
IS ISSUED

I. DEPOSITOR	II. IDENTIFICATION OF THE MICROORGANISM
Name:  Address: AS ABOVE	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY:  NCIMB 40814 Date of the deposit or of the transfer:  9 July 1996
III. VIABILITY STATEMENT	
The viability of the microorganism identified under II above was tested on 11 July 1996 <sup>2</sup> . On that date, the said microorganism was <input checked="checked" type="checkbox"/> <sup>3</sup> viable <input type="checkbox"/> <sup>3</sup> no longer viable	

<sup>1</sup> Indicate the date of the original deposit or, where a new deposit or a transfer has been made, the most recent relevant date (date of the new deposit or date of the transfer).

<sup>2</sup> In the cases referred to in Rule 10.2(a)(ii) and (iii), refer to the most recent viability test.

<sup>3</sup> Mark with a cross the applicable box.

IV. CONDITIONS UNDER WHICH THE VIABILITY TEST HAS BEEN PERFORMED<sup>4</sup>

INTERNATIONAL DEPOSITARY AUTHORITY

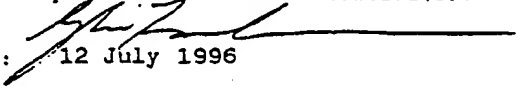
Name:

**NCIMB Ltd**

Address:

**23 St Machar Drive  
Aberdeen Scotland  
UK**

Signature(s) of person(s) having the power  
to represent the International Depositary  
Authority or of authorized official(s):

Date:  12 July 1996

<sup>4</sup> Fill in if the information has been requested and if the results of the test were negative.



Zeneca Limited,  
Jealott's Hill Research  
Station,  
Bracknell,  
Berkshire.  
RG12 6EY

BUDAPEST TREATY ON THE INTERNATIONAL  
RECOGNITION OF THE DEPOSIT OF MICROORGANISMS  
FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT  
issued pursuant to Rule 7.1 by the  
INTERNATIONAL DEPOSITARY AUTHORITY  
identified at the bottom of this page

NAME AND ADDRESS  
OF DEPOSITOR

<b>I. IDENTIFICATION OF THE MICROORGANISM</b>	
Identification reference given by the DEPOSITOR:  lambda phage banana cDNA library U2	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY:  NCIMB 40814
<b>II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION</b>	
The microorganism identified under I above was accompanied by:  <input type="checkbox"/> a scientific description  <input checked="" type="checkbox"/> a proposed taxonomic designation  (Mark with a cross where applicable)	
<b>III. RECEIPT AND ACCEPTANCE</b>	
This International Depositary Authority accepts the microorganism identified under I above, which was received by it on 9 July 1996 (date of the original deposit) <sup>1</sup>	
<b>IV. RECEIPT OF REQUEST FOR CONVERSION</b>	
The microorganism identified under I above was received by this International Depositary Authority on (date of the original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on (date of receipt of request for conversion)	
<b>V. INTERNATIONAL DEPOSITARY AUTHORITY</b>	
Name:  <b>NCIMB Ltd</b> 88 Macfar Drive Aberdeen Scotland AB9 8QY	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s):  Date: 12 July 1996

<sup>1</sup> Where Rule 6.4(d) applies, such date is the date on which the status of international depositary authority was acquired.